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June 2, 2004, 15:24:48; Search time 652 Seconds (without alignments) 3988.623 Million cell updates/sec
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                                                                                                                                                                                           3470272 seqs, 21671516995 residues
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AX137738 Sequence	AX137739 Sequence	AX137736 Sequence	AX13//43 Sequence AX137747 Sequence	AX137751 Sequence	VOILLS Minute viru	J02275 Minute viru	U34233 MOUSE DAIVO	U34256 Mice minute	M12032 Minute viru	X02481 Mouse parvo	U34254 Mouse parvo	M81888 parvovirus	L20503 Parvovirus	AF317513 Autonomou	AF036711 Kilham ra	AF332882 KAC MINUC	AF321230 Kilham ra	U79033 Kilham rat	AF332884 Rat minut	AL671965 Mouse DNA	AL606756 Mouse DNA	AB000048 Feline pa	ABUNUN49 FELINE DA	AB000051 Fellie pa AB000053 Feline pa	AB000055 Feline pa	AB000057 Feline pa	AB000060 Feline pa	AB000062 Feline pa	AB000063 Feline pa	AB000065 Feline pa	ABOOOOS FEILING DA	M10824 Feline panl	X55115 Feline panl	AR043629 Sequence AR043630 Sequence	D26079 Canine parv			DNA linear PAT 30-MAY-2001				ae; Farvovirinae; Farvovirus.	; tiftung des Oeffentlichen Rechts	
SUMMARIES	ID	AX137738	AX137739	AX137736	AX137743 AX137747	AX137751	PAMVM2		n vo	MVU34256	O		MOU34254	PVRSEO	PVRBBWOR	AF317513	AF036711	AF332882	AF321230	KRU79033	AF332884	AL671965	AL606756	AB000048	AB000049	AB000053	AB000055	AB000057	AB000058 AB000060	AB000062	AB000063	AB000065	ABOOODE	PVFVP	PAFPVNS1	AR043629 AR043630	PVCY1A	ALIGNMENTS		60 bp	70743	911		es; Farvoviridae;	ommelaere,J. ariants 60-A 3 21-FEB-2001; orschungszentrum Stiftung	
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Sequence 8 from Patent EP1077260.
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AX137743.1 GI:14273917
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Best Local Similarity 98.3
Matches 59; Conservative
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Parvovirus nsl variants
Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 60; Conservative 0; Mismatches 0;
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Sequence 4 from Patent EP1077260.
AX137739.1 GI:14273913
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Parvovirus ns1 variants
Batent: Ep 1077260-A 8 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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                                                                                                                                                                    셤
                                                                                                                                                                                        / db_xref="Rafferball: CAC39993"
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| tspprdgofflsdsdsgryftkegrehlusklytythydeggentlkktis
| qtkkevsikttkelvhkkytyspedwhmqoposylemaypvkvchalcylthydergeithydergogynygythytyttkelthydergeithydergogynygythythytthydergeithydergogynygythythytthydergeithydergogynygysthasycakwgkydwsbwsenwab
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QVNQFKA I CSGQTI R I DQKGKGSKQI EPTPVI MTTNENI TVVR I GCEERPEHTQP I RD
RMLNI HLTHTL PGDFGLVDKNEWPMI CAWLVKNGY QSTWASYCAKWGKVPDWSENWAE
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNVQLTPAERIKLREIAEDNEWYTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETVTTAQETKRGRI
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ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGWNYVKVCHAICCVLNRQGGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 30-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nueesch,J. and Rommelaere,J.
Parvovirus nsl variants
Patent: EP 1077260-A 12 21-FEB-2001;
Dettsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                                                                  /note="unnamed protein product"
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                                                     'note="Parvovirus NS1 variant"
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Sequence 12 from Patent EP1077260.
AX137747
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                                                                                                                           /codon start=1
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AX137747
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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ORIGIN

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ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARTKTAFDLILEKAETSKLTRFSLPDTRTCR. FAFHGWNYVKYCHAICCVLNRQGGKR
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Patent: BP 1077260-A 16 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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                                                                                                                               1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG 60
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Minute virus of mice with two major open reading frames (genome).
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Mice minute virus
Mice minute virus
Viruses; sBDNA viruses; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mice minute virus
Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
                                                                                                                                                                 HILL TATABABACTACACTTABABGAGCTGGTGCATABABGAGTAACCTCACAGAG
                                                                        Gape
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Score 58.4; DB 6; Length 2019;
Pred. No. 2.7e-09;
0; Mismatches 1; Indels 0.
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                                                                                                                                                                                                                                                                                                                                     linear
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/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                        DNA
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                                                                                                                                                                                                                                                                                                                        Sequence 16 from Patent EP1077260.
AX137751
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         97.3%;
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V01115.1 GI:60911
            Query Match
Best Local Similarity 98.3
Matches 59; Conservative
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CDS

FEATURES

COMMENT

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RIKLREIABDNEWYLTLTYKHKQTKKOYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1LEKAETSKLTNFSLPDTRTCRIFAFHGMNYYKYCHAICCVLRRQGGKRNTVLFHGPA
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TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
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SRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAARVERA
                                                                                                                                                                                                                                                    is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; Protein sequence is in conflict with the conceptual translation; coding sequence"
                                                                                                                                                                                                                   The messenger RNA of this virus (colinear with the strand listed)
Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2286. .2354
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(db_xref="GQA:P03137"

(db_xref="SALSS-PROT:P03137"

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                                                                                                         Nucleic Acids Res. 11 (4), 999-1018 (1983)
                                                                                                                                                                                                                                                                                                                                                                                           'organism="Mice minute virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114. .2279
                                                                            parvovirus
                                                                                                                                              83143341
                                                                                                                                                                                  6298737
                                                                                                                                                                                                                                                                                                                                                                     source
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CDS

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Original source text: Minute virus of mice (strain MVM(p)), passed in mouse 1 (variant A-9) cells.

Original source text: Minute virus of mice (strain MVM(p)), passed in mouse 1 (variant A-9) cells.

The parvoviridae family cantains two groups that infect mammalian hosts: (i) defective (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-independent) parvoviruses. MVM is a member of the latter group. Both groups have been demonstrated to package both plus and minus strands (in separate particles) of the ssnDNA aponome, though the minus strand is more typically packaged in the latter group.

The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

The 3' and 5' termini both exhibit the potential for forming stable for iteration.
SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILI
NANPIGTKNDIHFSNVFNSYGPLTAFSHSPYYYDGQLWDKELDLEHKRRLHITARFY
CKNNAPGQMLVRLGPNTJDQYDPNGATLSRYYTYGTFFWKGKLTMRAKLRANTTWNPV
YQVSAEDNGNSYMSVTKWLPPARGNQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                        1101 GAAGTTTCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGGGTAACCTCACCAGGG 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRL 22-MAY-1995
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The left and right halves of the genome encode two distinct, but overlapping transcriptional units. The transcripts can be summarized [1] (1 map unit (mu) = 51 bp):

R1 (4.8 kb): 4.5 mu - 46 mu; 46+ mu - 95 mu
R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 (3.0 kb): 40 mu - 46 mu; 46+ mu - 95 mu
R3 is the major transcript.

R3 is the wajor open reading frames, both on the plus (or C) There are two major open reading frames, both on the plus (or C) afternd. The left side ORF (261-2279) probably encodes a non-capaid protein of 85 kd; the right side ORF probably encodes the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs J. Virol. 60 (3), 1170-1174 (1986) 87061199
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5149)
Satell,C.R., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5149)
                                                                                                                                                                                                                                                                                           1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                           Length 5081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J02275 M12520 M12521 M14704
J02275.1 GI:332293
alternative splicing; capsid protein; complete genome;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                           Score 58.4; DB 14;
Pred. No. 2.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 11 (4), 999-1018 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVMPCG 5149 bp ss-DNA Minute virus of mice, complete genome.
                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prototype strain
J. Virol. 57 (2), 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morgan, W.R. and Ward, D.C.
                                                                                                                                                                  97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonstructural protein.
                                                                                                                                                                                                                                   59; Conservative
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Mice minute virus
                                                                                                                                                                                                  Best Local Similarity
Matches 59; Conserv
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GTSGVSRAGKRTRPPAYI FI NQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAA
RVERAADGPGGSGGGGGGGGGGGGGGSTRLYRPLGDGWVEI TALATRLVHLNMP
KSENYCR I RVHNTTDTSVKGNMAKDDAHEQI WTPWSLVDANAMGVWLQPSDWQY I CNT
                                                                                                                                                                                                                                                                                                                                                                                                                                            MSQLNIJVSLDQEI FNVVLKTYTEQDLGGQÄIKIYNNDLTACMMVAVDSNNILPYTPAA
NSMETLGFYWKPTIASPRYKYCVDRDSLGYTPANDGGTYBHVWGTPKGMNSQFFTI
NSMOTILLRTGDEFATGTYYPDTNSVKLTHFWQTNGLGQPPLLSTPPRADAGTT
TAQGSRHGTTQMGVNWYSEAIRTRPAQVGFCQPHNDFBASRAGPPAAPKVPADITGGV
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GSYDNQTHYRRLGDGWVBITALATRLVHINMPKSENYCRIKYHTYTDSYKGNWAKDD
AHEOIWTPWSLVDANAWULQPSDWYCICUTWSQLALVSLDQEIFNYVLKTTBQDL
GGQAIKIYNNDLTACMWVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYPCVD
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LINDILINNADTGTKNDIHFSNVFNS VOSUTARENBSPYYDGOQUWDKELDLEHKRPLH
LINDEVCKNNAPGQNLARLGPULTDOYDPNGATLSRIVTYGTFFWKGKLTWRAKLRAN
TTWNPVYQVSAEDNGNSYMSVTKWLPTATGNMOSVPLITRPVARNTY"
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QVGFCQPHNDFEASRAGPFAAPKVFADITQGVDKEANGSVRYSYGKQHGENWASHGPA
                                                                                                                                                                                                                                                                                                           trānslation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE"
                                                                                                                                                                                                                                                                                                                                        AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.3%; Score 58.4; DB 14; Length 5149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ORF1; putative"
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/protein_id="AAA67110.1"
/db_xref="GI:825482"
/translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                                              /note="alternative intron"
join(2286. .2316,2399. .4557)
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MFNYLFYRPEITWF"
2399. .>4557
/gene="VP1"
                                                                                                                                                                                 join(2286. .2316,2399. .4557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORF3; putative"
/codon_start=1
/product="unknown protein"
/protein_id="AA467112.1"
/db_xref="G1:825483"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown protein"
/protein_id="AAA67113.1"
/db_xref="GI:825484"
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/db_xref="G1:332296"
                                                                                                                                                                                                                                                             /proteIn_id="AAA67111.1"
/db_xref="GI:332294"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORF2; putative"
/codon_start=1
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/gene="VP"
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/gene="VP"
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/gene="VP"
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/gene="VP"
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/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="VP2"
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capsid proteins, VP1 (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron bundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2]
[3] sites; splice RIFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELKSLQRGAETTWDQSEDMEWETTVDEMTKKQVFIFDSLVKKCLFEVLNTKNIFPGD
VNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTACNVQLTPAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
ILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKRNTVLFHGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / train lation="MAGNAYSDEVLGATWMLKEKSNQEVFSFVFKNENVQLNGKDIGW
NSYKKELQEDELKSLQRGAETTWDGSEDMEWETTVDEMTKKGVFIFDSLVKKCLFEVL
NSYKKELQEDELKSLQRGAETTWDGSEDMEWETTVDEMTKKGVFIFDSLVKKCLFEVL
NTKNIFPGEDVUMFVQHEWGENGGWHCVLJGGKDFSQAGKWWRRQLNVYWSRMLYTA
CNYQLTPAREI LETAEDMEWYTLLTYKHKGTKKDYTKCVLFGNMLAYYFLTKKKIS
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTKKEVSIKTTLKELVHKRVTSPEDMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLINFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVNQPKAICSGQTIRIDÖKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRD
MRINIHLTHTLEGDFGLYVDKREWPHICAMLVTKORYQSTWASVCAKWGKVPDWSENWAE
PKVPTPINLLGSARSPETTPRKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEBDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MISGSGSLNQGAKRKWAWFKVYKQLLKSVTYLFPHSVSRDAQKE
SNQLTWAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGWNSYKKELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIMVEEAGNFGQQVNQFKAIC
SGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRDRMLNIHLTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKLREIAEDNEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLPGDFGLVDKNEWPMICAWLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINL
                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:10794"
|lab_host="mouse | (variant A-9) cell"
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/db_xref="GI:332295"
                                                                                                                                                                                                                                                                                     organism="Mice minute virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA67108.1"
/db_xref="GI:825481"
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/strain="MVM(p)"
                                                                                                                                                                                                          sites; splice sites.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="putative"
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/gene="VP"
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/gene="VP"
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NNYKKELQEDELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVF1YDSLVKKCLFEVL
STKN1APADVTWFVQHEWGKDQGWHCHVL1GGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLTPAER1KLRE1AEDSEWVTLLTYKHKQTKKDYTKCVLFGNM1AYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                            OVNOFKA I CSGQTIR I DÖKGKGSKOI EPTPVIMTTNENI TVVKI GCEER PEHTOP I RD
RMLNIHLTHTL PGDFGL VDKNEWPMI CAML VKNGYQS TWASYCAKWGKVPDWTENWAE
PKVPTP I NSLGSARS PFTTPKSTPLSQNYAL TPLASDLEDLALEPWSTPNTPVAGTAE
                                                                                                                                                                                                                                                                                                                            TSPPRDGGYPLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
KYKEKSVSIKTTLKELVHKRYTSPEDMMMQPDSY IEMMAGGGERLLKRYTLEICTUTL
ARTKTAFDLI LEKAETSKLTNRFSLPDTRTCK FAFHGMYTIKVCHAICCVLNRGGGKR
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/organism="Mouse parvovirus 1"
(mol_type="genomic DNA"
(mol_type="genomic DNA"
(mol_type="genomic DNA"
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                                                                                                                                                                                    /product="nonstructural protein 1"
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/gene="NS1"
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                                                                                       1101 GAAGTTTCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCCAGAG 1160
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1 (bases 1 to 4764)

Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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(bases 1 to 5144)

Ball-Goodrich, L.J. and Johnson, E.

Molecular characterization of a newly recognized mouse parvovirus

J. Virol. 68 (10), 6476-6486 (1994)
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
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                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mouse parvovirus lb"
/mol type="genomic DNA"
/specific_host="Mus musculus"
/db_xref="taxon:42841"
    Pred. No. 2.4e-09;
0; Mismatches 1
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Ball-Goodrich, L.J.
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Mouse parvovirus 1b
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RVERAADGPGGSGGGGGGGGGVGVSTGSYDNQTHYRPLSDGWVEITAYSTRMVHLNMP
KSENYCRVRVHNTNDTRTAGNMAKDDAHEQIWTPWSLIDSNAMGVWFQPSDWQFICNN
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NTQRIQLLRTGDEFATGTYYFETEPIKLSHTWQSNRQLGQPPQITDLPTADNENATLV
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AYDKYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPRLASSSEP
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NNILTNSDPIGNKTAIHYQNVFNSYGPLTAFPHPAPIYPQGQIWDKELDLEHKPRLHA
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TWNPVYQVSAQYQNENEYMSIHKWLPTATGNMQSIPLLSRPVARNTY"
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Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt. 5), 899-911 (1996)
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Mice minute v
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90.3%; Score 54.2; DB 14; Length 5144;
Best Local Similarity 94.9%; Pred. No. 6.4e-08;
Matches 56; Conservative 0; Mismatches 3; Indels 0;
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Join(2290, .2320,2403. .4561)
/gene="VP1"
                                                                                                                                                                                                                                                                                            /product="capsid protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Original source text: Minute virus of mice (lymphotropic variant of MVM) DNA, clone pBG222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRL 05-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MISGSESIDQGAKRKWAWFKVYKQMIKSVTYPFFHSVSRDAQKE
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DELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVFIYDSLVKKCLFEVISTKNIAPAD
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ILEKAETSKLTNFSLPDTRTCKIFAFHGWNYVKVCHAICCVLNRQGGKRNTVLFHGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRDRMLNIHLTH
TLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAEPKVPTPINS
LGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTACNVQLTPAE
RIKLREIAEDSEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Astell, C.R., Gardiner, B.M. and Tattersall, P. DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5085)
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                     Submitted (17-AUG-1995) David G. Besselsen, Department of Submitted (17-AUG-1995) David G. Besselsen, Department of Veterinary Pathology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA
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                                                                                                                                                                                                                                                                                                                                         Query Match 87.7%; Score 52.6; DB 14; Length 4761; Best Local Similarity 93.2%; Pred. No. 2.2e-07; Matches 55; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alternative splicing; capsid protein; complete genome; nonstructural protein. Mice minute virus Mice minute virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                specific host="Mesocricetus auratus"
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J. Virol. 570, 656-669 (1986)
86115415
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115. .2280
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2 (bases 1 to 4761)
Besselsen, D.G.
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                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
MVMICG
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VERSION
KEYWORDS
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TITLE
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MEDLINE
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                            AUTHORS
    REFERENCE
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STKNI APADVTWEVOHEWGKDGGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRMLVTA
CNVQLTPAER I KLREI AEDSEWVTLLTYKHKQTKKDYTKCVLFGNMI AYYFLTKKKI S
TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETVTTAQETKRGRI
                                                                                                                                                                                                                                                                                                                                                                                                  ARTKTAFDLILEKAETSKLTNFSLPDTRTCKI FAFHGWNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEBAGNFGQ
QVNQFKAICSGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRD
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKRDFSEPINLD"
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ENTQOITLENTGDERFATGYYZFDTWRYLTHTWYDRQLGGPPLLSYPERADTDAGTL
ENTGOSRHGATGWEVMWSER1RTRPRQVGFCOPHNDFEASRAGPFAARVPADVTQGY
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ITAPPVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRI VTYGTFFWKGKLTMRAKLRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
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2003. .2281
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|note="minor transcription start site"
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/gene="VP1"
join(2287. .2317,2400. .4558)
/gene="VP1"
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DRDLSVTYENQEGTIEHNVMGTPKGWNSQFFIIENTQQITLLKTGDEFATGTYFFDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPPAYIFINQARAKKKITSSAAQQSSQTMSDGTSQPDGGNGVHSAARVERAADGPGGS
GGGGSGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIDTSVKGNMAKDDAHEQIWTPWSLVDANAMGVWLQPSDWQYICNTWSQLNLVSLDQE
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EVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKOHGENWAAHGPA ERYTWDETNFGSGRDTRDGFI OSAPLVVPPPLNGI LTNANPIG
TKNDI HFSNVFNSYGPLTAFSHPSPVYPQGQI WDKELDLEHKPRLHI TAPFVCKNNAP
GOMLVRLGPNLTDQYDPNGATLSRI VTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVKLTHTWOTNROLGOPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRP
AQVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNS
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QYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
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Data kindly reviewed (18-JUL-1986) by G. McMaster.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
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93.2%; Pred. No. 2.2e-07;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="terminal hairpin region"
                                                                                                                                                                note="terminal hairpin region"
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Best Local Similarity
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DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANYMI 5087 bp DNA linear VRL 01-JUL-1999 Mouse parvovirus minute virus immunosuppressive variant genome ( =
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PBRYTWDETHYGSGRDTRDGFTQSAPLVVPPPINGTILTNANPTGTKNDTHFSNVFNSY
GPLTAFSHPSDFVYPQCQIUMKELLDLEHKPRLHTTAPPVCKNNAPGQMLVRLGFNLTDG
YDPNGATLGSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWLP
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Mice minute virus
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                                                                                                                                               /codon_start=1
/product="unknown protein"
/protein_d="AAA69570.1"
/db_xref="G1:825479"
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'db_xref="GI:825480"
                                                         'note="alternative intron"
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/db_xref="GI:332292"
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/codon_start=1
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/gene="VP1"
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/gene="VP1"
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/gene="VP2"
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/gene="VP2"
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VRL 21-AUG-1996
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Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Hamster parvovirus
Viruses; Barvoviridae; Parvovirinae; Parvovirus.
Viruses; BaDN viruses; Parvoviridae; Parvovirus.
1 (bases 1 to 4773)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt. 5), 899-911 (1996)
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Submitted (17-AUG-1995) David G. Besselsen, Department of Veterinary Pathology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA Location/Qualifiers
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91.5%;
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Besselsen, D.G.
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Mouse parvovirus 1c
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                               Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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** **	Aav52148 Streptoco Adc85298 Human Egr Ada02819 Mouse Sos Adb72557 Mouse Sos	Continuation (21 o Abl32795 Human imm Ach36399 Human end	Aca23159 Cone Acazyot Continuation (3 of Aav52850 Human eya Ada02843 Mouse Fgf	Adb72581 Mouse Fgf Adc85322 Human Map Continuation (4 of Continuation (5 of	Abn95790 Gene #228 Abn67384 Streptoco Continuation (12 o
AAX30921 ABX50132 ABX08031	AAV52148 ADC85298 ADA02819 ADB72557	ABS56454_20 ABL32795 ACH36399	ACA23159 AAX20248_02 AAX52850 ADA02843	ADB72581 ADC85322 AAV21209 03 AAV21209 04	ABN95790 ABN67384 ABN71527_11
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ALIGNMENTS

/*tag= b /note= "This location corresponds to position 847 of the NS1 variant (S283A) DNA shown in AAD02799" Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity. NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds. Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA fragment. /*tag= a product= "Parvovirus NS1 variant (S283A) peptide" /note= "CDS does not include start and stop codon" (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. Location/Qualifiers replace (7, A) 99EP-00115161 99EP-00115161 (first entry) /partial Rommelaere (revised) WPI; 2001-212717/22. P-PSDB; AAY72703

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Matches

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The present sequence is a DNA encoding parvovirus non-structure protein 1 (NS1) variant (1363A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cyctocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-NUG-2003 to correct OS field.)
                                                                                                                                                                                             841 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGGATAAAAGAGTAACCTCACCAGAG 900
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                                                                                                                                                                   1 GAAGTIGCTATIAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parvovirus non-structure protein 1 (NS1) variant (T363A) DNA.
                                                                                   Length 2019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                       Sequence 2019 BP; 698 A; 389 C; 453 G; 479 T; 0 U; 0 Other;
                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "NSI variant (T363A) protein"
replace(1187, A)
/*tag= b
therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                 Score 60; DB 5;
Pred. No. 8.6e-12;
                                                             100.0%; Sco...
100.0%; Pred. No. c...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                           60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2019
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P-PSDB; AAY72706.
                                                                                   Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1999;
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  AAD02801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                  SXS
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                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                             The present sequence is a parvovirus non-structure protein 1 (NS1) variant ($283A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-NUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                               GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG
                                                                                                                                                                                                                                                                                                                                                                  1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG
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                                                                                                                                                                                                                                                                                   DB 5; Length 60;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "NS1 variant (S283A) protein"
replace(847, A)
                                                                                                                                                                                                                                       Sequence 60 BP; 24 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       4.2e-12;
                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                 100.0%; Score 60;
100.0%; Pred. No.
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                            Disclosure; Page 11; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 11-14; 41pp; English
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                                                                                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                                                                                             60; Conservative
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Best Local Similarity
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31-MAY-2001
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mutation

X Y Y Y B Y B

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/*tag= a /product= "NS1 variant (T394A) protein"

replace(1180, A) /*tag= b

99EP-00115161 99EP-00115161

Rommelaere J;

Location/Qualifiers 1. .2019

(first entry)

(revised)

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Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and
                                                                  NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gené therapy; mutant; mutein; variant; ds.
                                             Parvovirus non-structure protein 1 (NS1) variant (T394A) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                       transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                  (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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             06-AUG-2003
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                         31-MAY-2001
                                                                                                                                                                                                                                                                                                                                         Nueesch J,
                                                                                                      Parvovirus
                                                                                                                   Synthetic
                                                                                                                                                                                       mutation
                                                                                                                                        Key
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  셤
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The present sequence is a DNA encoding parvovirus non-structure protein (NSI) variant (1463A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-ANG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                         NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                   Parvovirus non-structure protein 1 (NS1) variant (T463A) DNA.
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                                                                                                                                                                                                                                                                     /*tag= a
/product= "NS1 variant (T463A) protein"
                                                                                                                                                                                                                                            Location/Qualifiers
1. .2019
                                                                                                                                                                                                                                                                                                                                                                                                                        (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                                                                                                                           replace(1387, A)
                                                                      AAD02805 standard; DNA; 2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.3%;
98.3%;
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                                                                                                                               (first entry)
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                                                                                                                   (revised)
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P-PSDB; AAY72710.
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Best Local Similarity
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31-MAY-2001
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                                                                                                                                                                                                            Parvovirus
                                                                                                                                                                                                                         Synthetic
                                                                                            AAD02805;
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                                       protein 1
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                                 The present sequence is a DNA encoding parvovirus non-structure protein (NS1) variant (T394A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                               1 GAAGTTGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAAGAGTAACCTCACCAGAG
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                           Length 2019;
                                                                                                                                                                                                   Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parvovirus non-structure protein 1 (NS1) wild-type DNA
                                                                                                                                                                                                                                         Score 58.4; DB 5;
Pred. No. 3.2e-11;
                                                                                                                                                                                                                                                                                  0; Mismatches
Claim 7; Page 22-24; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD02797 standard; DNA; 2019 BP
                                                                                                                                                                                                                                       97.3%;
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(first entry)
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Best Local Similarity 98.3
Matches 59; Conservative
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31-MAY-2001
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Gaps ; 0

1; Indels

0; Mismatches

59; Conservative

Matches

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9

841 GAAGTTTCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG 900

AAD02803 standard; DNA; 2019

AAD02803

AAD02803 ID AAD XX . RESULT

1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG

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Gaps

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59

Key

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11116 GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
                                                                                                                                             This viral DNA is isolated from a non- attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEMSZ. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                               relative to control
disease in animals,
                                                                                                                                                                                                                                                                                                                                                                1 GAAGTIGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA
                                                                                                                                                                                                                                                                Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               Score 28.6; DB 2; Length 5049;
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                               19; Indels
                                               Attenuated CPV strains contg. up to 4 mutation (s) virus - useful as a veterinary vaccine against CPV such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Attenuated canine parvovirus CPV~39 passage 60 DNA.
                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                Claim 1; Page 21-24; 42pp; English.
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67.88;
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Best Local Similarity 67.00
Best A0; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parvovirus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a wild type DNA encoding parvovirus non-
structure protein 1 (NS1). The present invention relates to the variants
of the parvovirus non-structure protein (NS1) having a shifted
equilibrium between the DNA replication and transcription activities, and
the cytotoxicity activity. These variants are useful as toxins for
treating tumoural diseases. The variant DNAs are useful as vectors for
gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                 Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 GAAGTTTCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGGTAACCTCACCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAAACCTCACCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58.4; DB 5; Length 2019;
Pred. No. 3.2e-11;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2019 BP; 698 A; 389 C; 452 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-attenuated canine parvovirus CPV-39 passage 5 DNA
                                                                                "Parvovirus NS1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parrish CR, Gruenberg A, Carmichael LE;
                                                                                                                                                                                                                                                  (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                             Location/Qualifiers
1. .2019
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT15311 standard; DNA; 5049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.3%;
                                                                                                                                                                                   99EP-00115161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US014207
                                                                                                                                                                                                                  99EP-00115161
                                                                  /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                   Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 98.3
les 59; Conservative
                                                                                                                                                                                                                                                                                                                 WPI; 2001-212717/22
P-PSDB; AAY72702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1994;
                                                                                                                  EP1077260-A1
                                                                                                                                                                                 13-AUG-1999;
                                                                                                                                                                                                                   13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9614088-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-1996
                                                                                                                                                 21-FEB-2001
 Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT15311;
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RESULT 7

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AAT88324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOS
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                                                                                                                                                                                                                                                                                                                            GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGGGTAAAAAGTGTAACTCACCTGA 1174
                                                 This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGB312 or pGEM52. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/note= "base 4307 is A in virulent CPV-39 (G in passage
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "base 4973 is C in virulent CPV-39 (T in passage 65 attenuated virus)"
                                                                                                                                                                                                                                                                                                 1 GAAGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "base 4358 is C in virulent CPV-39 (T in passage 55 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (T in passage
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (A in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parvovirus; CPV; attenuation; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
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                                                                                                                                                                                    Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                                                                                                                                                                                                                      47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 2.4;
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/note= "base 4889 is C in virulent CPV-39
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= f
/note= "base 4477 is G in virulent CPV-39
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= e
/note= "base 4409 is_C in virulent CPV-39
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/note= "NS1/NS2 coding region"
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/note= "VP1/VP2 coding region"
4307
                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                     Claim 2; Page 24-27; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT88321 standard; DNA; 5049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                            40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parvovirus
                                                                                                                                               canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1998
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                                                                                                                                                                                                                                                                                                                                     1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT88321;
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canine
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
AAT88321
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- used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Attenuated viruses are obtained by serial passage of the virulent CPV type 2b isolate 39 in NLFK feline kidney host cells. They have one or more of the sequence alterations indicated in the sequence relative to the sequence of a control (5th passage) wild-type CPV-2b (see AAT88320). A claimed virus from the 65th passage (deposited as ATCC W 2528) contains all 6 mutations. The DNA from attenuated CPV strains (see also AAT88324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against feline patheukopenia virus and mink enterties virus. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1116 GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGTIGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA
                                                                                                                                                                                                                     canine parvovirus DNA carrying specific attenuating mutation(s) - use vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d "base 97 is C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine parvovirus; CPV; attenuation; vB1440; vaccine; dog;
feline panleukopenia virus; mink enteritis virus; infection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5049 BP; 1788 A; 809 C; 1029 G; 1417 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G in CPV-39 (passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Attenuated canine parvovirus (vBI440) genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "VP1/VP2 coding region"
4745
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note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parvovirus; vBI440 (ATCC VR 2489).
                                                                                                                       Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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"base 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT88324 standard; DNA; 5049 BP
                                                          (CORR ) CORNELL RES FOUND INC
96US-00647655
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence given in AAT88320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 67.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2286.
                                                                                                                                                                                     WPI; 1998-008583/01
15-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2003
21-MAY-1998
                                                                                                                       Parrish CR,
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parvovirus; CPV; attenuation; vBI440; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                          Canine parvovirus 39 passage #5 (wild-type).
                                                                                                                                                                                                                                                                                                                                                                                                                       Canine parvovirus; type 2b isolate 39.
                                                                                                                                          Example 8; Page 34-37; 60pp; English.
                                                                                (CORR ) CORNELL RES FOUND INC
                                                         97WO-US007584.
                                                                                                                                                                                                                                                                                                                                                  AAT88320 standard; DNA; 5049
                                                                     96US-00647655
                                                                                                                                                                                                                                                                                        67.8%;
                                                                                            Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                               40; Conservative
                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                        WPI; 1998-008583/01
                                                                                                                                                                                                                                                                                        Local Similarity
                                                          06-MAY-1997;
                                   WO9742972-A1
                                                                                            Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2003
21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                              AAT88320;
                                                                                                                                                                                                                                                                                                                      1116
                                                                                                                                                                                                                                                                                    Query Match
            mutation
                                                                                                                                                                                                                                                                                                                                                                                                       Canine
                                                                                                                                                                                                                                                                                                                                                                                                            feline
                                                                                                                                                                                                                                                                                          Best Loca
Matches
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This DNA sequence comprises the genome of virulent canine parvovirus type 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline kindey host cells. Further passaging has yielded attenuated virus vBI440 (ATCC VR 2489) (see AAT88324) from the 66th passage, and a claimed virus (see AAT88321) derived from the 65th passage, and a claimed virus (see AAT88321) derived from the 65th passage (ATCC 2528). These stages virus. The DNA from attenuated CACC 2528) is used for the passage virus. The DNA from attenuated clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The cattenuated viruses can be used in dogs as a vaccine to protect against cattenuated viruses and mink entertis virus. The vaccines protect against feline panleukopenia virus and mink entertis virus. The vaccines protect against the currently prevalent cattains of types 2 and 2a), and provide a long term immune response. (Updated on 17-007-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1116 GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAGTIGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.7%; Score 28.6; DB 2; Length 5049; Best Local Similarity 67.8%; Pred. No. 2.4; Matches 40; Conservative 0; Mismatches 19; Indels 0.
                                                                           coding region'
                                                                                                                                                 /note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 37-40; 60pp; English
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prokaryotic essential gene #9353.
                                                   /*tag= a
/note= "NS1/NS2
2286. .4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACA27696 standard; DNA; 2931 BP
                                                                                                                                                                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                     97WO-US007584.
                                                                                                                                                                                                                                                                                                                                                      96US-00647655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2003 (first entry)
                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-008583/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug design; gene
                                                                                                                                                                                                     WO9742972-A1.
                                                                                                                                                                                                                                                                                                     36-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                      15-MAY-1996;
                                                                                                                                                                                                                                                   20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA27696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
Key
                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACA27696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This DNA sequence comprises an attenuated virus genome derived by serial passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate 139 in NLEK feline kidney host cells. The attenuated virus is designated value (ATCC VR 2489). It contains 4 mutations relative to the sequence (see AATB8320) of the control (5th passage) wild-type CPV-2b. 2 Mutations are within the hairpin formed by the 3' terminal palindrome: the mutation cross are within the hairpin formed by the 3' terminal palindrome: the mutation cross at nucleotide 59 introduces an A into a G-C rich region within the tip of the hairpin, disrupting the base pairing in one of the 2 small internal control the mismatched bubble (flip-flop) sequence within the control palindrome. The DNA from attenuated CPV strains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in the palindrome transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus DNA carrying specific attenuating mutation(8) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGIGICAAICAAIGIACITIGGGGGACITIGGITAGIAAAAGAGIAACAICACCIGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 2.4;
/*tag=  e
/note= "base 4745 is T in CPV-39 (passage 5)"
                                                                        /*tag= f
/note= "base 4881 is C in CPV-39 (passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Gruenberg A;
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Gaps , 0

Clostridium acetobutylicum

WO200277183-A2

03-OCT-2002

Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.

Gene #2617 used to diagnose liver cancer.

```
the invention relates to an isolated mucieic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producting the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confidention or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation of an organism acts; (9) manufacturing an entibiotic; (10) profiling a compound that inhibits proliferation of the test compound that inhibits proliferation of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains is present in a culture or collection of solutifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational chief drug discovery programs, or for screening homologous nucleic acids are useful for required for proliferation or or solate candidate molecules for rational crossors are not better acids are useful.
                                                                                                                                                                                                                                                                                                                                                                                              screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at 100.
                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2931 BP; 1135 A; 299 C; 597 G; 900 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                    Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; SEQ ID NO 15566; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                                                                     2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                  2001US-00815242
                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                          2002US-0362699P
                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                       WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABU23826
                                                                                     06-SEP-2001; 25-OCT-2001; 08-FEB-2002;
                                                                  21-MAR-2001;
                                                                                                                                                            06-MAR-2002;
                                                                                                                                                                                                                                                    Wang L,
Wall D,
```

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN03503-ABN09455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, array forsity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

Claim 1; SEQ ID NO 2617; 298pp; English

Vocklev JG:

Peres-Da-Silva S,

Alvares C,

Horne D,

WPI; 2002-426119/45.

(GENE-) GENE LOGIC INC

02-OCT-2001; 2001WO-US030589 02-OCT-2000; 2000US-0237054P

WO200229103-A2

11-APR-2002

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0; Gaps

Sequence 388 BP; 139 A; 68 C; 66 G; 115 T; 0 U; 0 Other;

[tp.wipo.int/pub/published_pct_sequences

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1 GAAGTTGCTATTAAAACTACACTTAAAGGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                      Acetyl-coenzyme-A-carboxylase; acetyl-CoA-carboxylase; ACCase; transgenic plant; oilseed; crop improvement; fatty acid; transgenic plant; oilseed; poly-beta-hydroxyalkanoate; poly-beta-hydroxyalkanoate; herbicide resistance; pesticide resistance; poly-beta-hydroxyalkanoate; herbicide resistance;
Query Match
42.3%; Score 25.4; DB 6; Length 388;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                        Arabidopsis ACCase clone pKLU81.
                                                                                                                                                                                      AAQ77691 standard; cDNA; 565
                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                        25-MAR-2003
08-MAY-1995
                                                                                                                                                                                                                       AAQ77691;
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                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                       1091 AAGAAGTAGTTAAAATACACTTAAAGAGCTTGTTAAAAATGGAATA 1137
                                                                                                                                                                                                                                          48
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                        2 AAGTTGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTA
                                                                                                                                                                        DB
                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                    Score 26.2; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                   vuery match
Best Local Similarity 72.3%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                           ABN96119 standard; DNA; 388
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Arabidopsis thaliana

(first entry)

13-AUG-2002 ABN96119;

ABN96119 XX ABN9 AC ABN9 XX AEN9 DT 13-A

RESULT 13

ò g

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A cDNA clone of rapeseed, identified as encoding ACCase, was used to probe a genomic library prepared from A. thaliana. The 5' sequence of an isolated subclone, pKLU81, was determined. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                              /*tag= d
/note= "base n at position 548 is not identified in the
specification"
556
                               a
"base n at position 483 is not identified in the
                                                                                                                       /*tag= c /note= "base n at position 526 is not identified in the
                                                                                                                                                                                                                  e
"base n at position 556 is not identified in the
                                                                                    in the
                                                                                                                                                                                                                                                                                                                                                                                                                       Plant DNA encoding acetyl coenzyme A carboxylase - used to transform plants to modify ACCase expression e.g. to increase poly:hydroxy-alkanoate prod, or herbicide resistance.
                                                                        *tag= b
note= "base n at position 494 is not identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 565 BP; 147 A; 98 C; 129 G; 186 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                             Fentem PA;
                                                                                                                                                                                                                                                                                                                                                                             Slabas A, Elborough KM, Bright SWJ,
        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 8; 47pp; English.
                                                                                                specification"
                                                     specification"
                                                                                                                                                                                                                                        specification
                                                                                                                                                                                                                                                                                                           94WO-GB000653
                                                                                                                                                                                                                                                                                                                                 93GB-00006490
                                                                                                                                                                                                                    /*tag=
                                tag=
                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-333188/41
                                                                                                                                                                                                                                                                                                                                                       (ZENE ) ZENECA LTD
                                                                                                                                                                                                    misc_difference
                    misc difference
                                                                 misc difference
                                                                                                             misc difference
                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                           29-MAR-1994;
                                                                                                                                                                                                                                                                                                                                  29-MAR-1993;
                                                                                                                                                                                                                                                               WO9423027-A2
```

/*tag= f /note= "unknown/unspecified residue"

Fentem PA

Slabas AR, Elborough KM, Bright SWJ,

(ZENE) ZENECA LTD.

94WO-GB000846. 94WO-GB000846.

21-APR-1994; 21-APR-1994; P-PSDB; AAR84623, AAR84622, AAR84624

WPI; 1995-382994/49

/*tag= e /note= "unknown/unspecified residue"

*tag= b 'note= "unspecified/unknown residue"

Arabidopsis thaliana; (clone pKLU81).

Location/Qualifiers

...268 *tag=

misc_feature

misc_feature

*tag= c note= "unspecified/unknown residue"

*tag= d note= "unknown/unspecified residue"

*tag=

misc_feature

misc feature

misc_feature

WO9529246-A1 02-NOV-1995.

```
The sequence represents the 5' end of subclone pKLU81 (NCIB 40555) encoding the Arabidopsis thaliana acetyl Coenzyme A carboxylase (ACCase) cDNA, which can be used to create a sense or an antisense expression cassette to transform rape and other oilseed plants (canola, soybean, sunflower) to downregulate production of the ACCase enzyme. The transgenic plants have a lower or a modified oil content. Down-regulation of il synthesis can be used to divert the substrate, acetyl Coenzyme A, into synthesis of alternative storage materials (starch, protein or novel polymers e.g. polyhydroxyalkanoates). Full-length ACCase clones can be used to create transgenic plants over-expression and therefore with increased oil content. ACCase over-expression in monocot plants such as wheat, barley, maize and rice, which are normally sensitive to herbicides, results in aryloxyphenoxy-propionate and alkylketone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herbicide resistance in the transgenic plants (dicots are normally resistant to these herbicides). (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding acetyl Coenzyme A carboxylase - used for developing plants with controlled expression of ACCase, e.g. for controlling fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 Trigererrakakereakerecrerrekakerrekakerkerakeeke 356
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 TTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 565 BP; 147 A; 98 C; 129 G; 186 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.3%; Score 25.4; 168.6%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthesis.
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Gaps

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Length 565;

DB 2;

0; Mismatches

Best Local Similarity 68.6 Matches 35; Conservative

Query Match

42.3%; Score 25.4; 68.6%; Pred. No. 22

TIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCAC 55

406

g 8

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AAT04949 standard; cDNA; 565 BP

RESULT 15 AAT04949/

2, 2004, 19:08:26 Search completed: June Job time : 149.25 secs

Acetyl Coenzyme A carboxylase; ACCase; plasmid pKLU81; transgenic plant; modified oil content; polyhydroxyalkanoate polymer; herbicide resistance; monocot crop improvement; ss.

Arabidopsis thaliana acetyl-Coenzyme-A-carboxylase 5' sequence.

(first entry)

(revised)

16-OCT-2003 02-JUN-1996

AAT04949;

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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AL168683 TELTAOODON BLI16316 RPCIT-24-3
BH068411 RPCIT-24-2
BH068411 RPCIT-24-2
BH068411 RPCIT-24-2
BH068411 RPCIT-24-2
BH068411 RPCIT-24-2
BH068411 RPCIT-24-2
BH06841237 BH0845324
AV122962 AV122015
AZ684019 ENTMJ20TF
AZ687690 ENTMJ20TF
CC146949 PULRAY4CTB
CC3419705 PURDEZ6TD
BC373420 PURDEZ6TD
BC373420 H068111 1
BU352437 G0352879
CC146949 PULRAY4CTB
CC358377 G0352879
CC383776 PURDEZ6TD
BU352437 G03528279
CC383415 BS811213
BU1341908 G03144628
BU341908 G03518113
BC180322 G0331171
BC22166 BOATO. FET
BU24128 G03144628
BU341908 G035813171
BC32166 BOATO. FET
BU24136 G03581317
BC32166 BOATO. FET
BU24136 G03184628
BU375185 G0358327
AZ437568 BU0255420
CC260400 CT4661-24L
AV530205 AV530205
BY607587 MA3-9999U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vitis vinifera
Vitis vinifera
Vitis vinifera
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis
1 (bases 1 to 687)
2 (Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAP0005_IVR_G02_Vitis vinifera_cv. cabernet sauvignon (Clone 8)
Petiole - CAP Vitis vinifera cDNA clone CAP0005_IVR_G02_3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
UC Davis, Plant Pathology
Tel: 530 754 6551
Fax: 530 754 6651
Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                           CNSOSFS3
BZ973479
BZ973479
BZ973483
CC3146949
CC358376
CC419705
BQ867043
AZ869268
BU352437
CD733420
                                                   BH068411
BJ438237
AV222962
AV142404
AV154012
BX453224
AX684019
AZ687690
CNS032B1
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BU304839
BU351446
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/lab_host="DH5alpha"
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                                                                                                                                                                                                                                                                      Once-Torgan: Periole, Vector: pDNR, Site 1: Sfil; Site 2: Sfil; CAP is a cDNA library of Vitis vinifera cv. Cabernet Sauvignon. Clone 8 petioles. Samples were collected on July 10, 2002 from plants on the onset of Veraison (berry softening). Sampled vines were located the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA12EI301IIR G12 Cabernet Sauvignon Leaf - CA12EI Vitis vinifera cDNA clone CA12EI301IIR G12 3', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
                                                                              /mol_type="mRNA"
/cultivar="Cabarnet Sauvignon"
/db_xref="taxon:29160"
/clone="CAPOIOS IVR G02"
/sex="Hermaphrodite"
/dev_stage="Onest of Veraison (berry softening)"
/lab_host="DH5alpha"
/clone lib="vytits vinifera cv. cabernet sauvignon (Clone B) Petiole - CAP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 777)
Goes da Silva,F., Lim,H., Iandolino,A., Baek,J., Jones,K.,
Walker,M.A. and Cook,D.R.
Transcriptional responses of Vitis vinifera to infection by the bacterial pathogen Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTACAGCCCAGCCGCGACATG-dT(30)NN-3'. Library wa
constructed using the Clontech Creator SWART tt and
size-selected to contain the 0.5-3 kb size fraction."
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/cultivar="cabernet Sauvignon"
/db_xref="txxon:29760"
/clone="CA12E13011IR_G12"
/sex="hermaphrodite"
/dev_stage="Mid-season leaf material"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UC Davis Department of Plant Pathology
1 Shields Ave., DAvis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                            'organism="Vitis vinifera"
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Seq primer: GCCAAACGAATGGTCTAG.
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CAES Genome Facility
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Gamal: schao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resggn.com). BAC end page:
http://www.tigr.org/tdb/bac.edu/mouse/bac_end_intro.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ246409 538 bp DNA linear GSS 15-JUN-2000
RPCI-23-92L24.TJ RPCI-23 Mus musculus genomic clone RPCI-23-92L24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tonnames, 1 to 538)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSS: RPCI-23-92L24.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 50.3%; Score 30.2; DB 14; Length 777; Best Local Similarity 69.5%; Pred. No. 12; Matches 41; Conservative 0; Mismatches 18; Indels 0.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-92L24"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/clone_lib="RPCI-23"
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Class: BAC ends.
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Bouneau, L., Fisher, C.,

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CNS01V5E 15P-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 197P20 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                            All68683. GI:7806740
All68683.1 GI:7806740
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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   RESULT 5
CNS01V5E/c
                                                                              LOCUS
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                                                                                                                                                 selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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/lab host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCACAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE300265 1018 bp mRNA linear EST 20-JUL-2000 000944030T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960382 3',
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
Cool: Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1018)

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMS3 row: k column: 07
High quality sequence start: 23
High quality sequence
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                   DB 28; Length 538;
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Pred. No. 46;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2960382"
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                                                                                                                                                                                                                                                                                                                                               ch 47.3%;
l Similarity 70.4%;
38; Conservative
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Best Local Similarity 70.4
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Best Local Similarity
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BE300265
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(bases 1 to 768)

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            Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.ons.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequenching project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/note="Genoscope sequence ID : COAG197DH10SP1~end
PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG
                                                                                                                                                                                                                                                                                                                                                                                       Length 768;
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                                                                                                                                                                 Location/Qualifiers
1. 768
/organism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                                                                                                       46.0%; Score 27.6; DB 29; 46.2%; Pred. No. 87;
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Mus musculus
                                                                                                                                                                                                                                                                        /clone="197P20"
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Genoscope
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Matches 2
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BH116316
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DEFINITION
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Gaps

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16; Indels

0; Mismatches

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7 GCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG

end

us-10-069-056-3.rst

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/cell type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ438237 Dictyostelium discoideum cDNA linear EST 13-MAR-2C
BJ438237 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv36f19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Clones are derived from the mouse BAC library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC e

page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: SP6

Class: BAC ends.
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1 (bases 1 to 760)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 45.7%; Score 27.4; DB 28; Length Local Similarity 75.6%; Pred. No. 99; Length 18. 34; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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/organism="Dictyostelium discoideum"
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/organism="Mus musculus"
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'strain="C57BL/6J"
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/clone="RPCI-24-227B7"
                                                                                                                                                                                                                                                                        Location/Qualifiers
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/strain="AX4"
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Dictyostelium discoideum
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BJ438237.1 GI:19412959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Male"
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 562)
S Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Praser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-227B7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male CS7BL/6J
DNA."
                                                                                                                                                                                                                                                                                                                                                                                Email: szladottgr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pdejongémail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 386 row: H column: 23
Seg primer: SP6
Class: BAC ends.
            Chordata, Craniata, Vertebrata, Buteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, I
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
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Pred. No. 88;
0; Mismatches 14; Indels 0;
                                                                                                                                                      Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other GSSs: RPCI-24-386H23.TV Contact: Shaying End Sequences Train and Faxyotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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/clone="RPCI-24-386H23"
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/strain="C57BL/6J"
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BH068411.1 GI:14888008
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                    Eukaryota, Metazoa,
Mammalia, Eutheria,
1 (bases 1 to 791)
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                                                                                                                                                                                                                                                                                                                        AV222962 RIKEN full-length enriched, 18 days pregnant, placenta and extra embryonic tissue Mus musculus cDNA clone 3830405E08 3' similar to X85183 R.norvegicus mRNA for ras-related GTPase, ragA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Transcriptional sequencing: A method for DNA sequencing using RNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                    Gaps
                                                                                                       4 GTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                               118 GTTAATGTTAAAGGTACAATTAGAGTTGTAGTTGATGAAGGTGTAATCTTACCAGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="placenta and extra embryonic tissue"
/dev_stage="18 days pregnant, adult"
/lab_host="DH10B"
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      Pred. No. 1.2e+02;
0; Mismatches 18; Indels
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/clone="3830405E08"
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/strain="C57BL/6J"
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67.98;
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                                    38; Conservative
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Thermostabilization and thermoactivation of thermolabile enzymes by Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninoi, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, M., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Yoshino, M., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., RIKEN Mouse ESTs
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                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 282)
                      Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                      primed with a primer [5′
GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3′],
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Tel: 81-298-36-9145
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Pred. No. 1.2e+02;
0; Mismatches 15
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/clone="2810423C19"
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/strain="C57BL/6J"
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Mus musculus
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1 Similarity 70.6%;
36; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-298-36-9098
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Kawij,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Itoh,M., Izawa,M., Izako,M., Sato,K., Shibata,Y., Shipamoto,Y., Shipata,Y., Shipata,Y., Shipata,Y., Shipata,Y., Shipata,Y., Shipata,Y., Shipamoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                    305 bp mRNA linear EST 08-JUL-199;
AVI54012 Mus musculus hippocampus C57BL/6J adult Mus musculus cDNA
clone 2900059G11, mRNA sequence.
AVI54012
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dev_stage="adult"
/clone_lib="Mus musculus hippocampus C57BL/6J adult"
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/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
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                                                                  Score 27; DB 9; Length 282; Pred. No. 1.3e+02; 0; Mismatches 15; Indels
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/mol_type="mRNA"
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/clone="2900059G11"
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Mus musculus
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1 Similarity 70.6%;
36; Conservative
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Fax: 81-298-36-9098
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AV154012/c
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RESULT 12 BY453224/c

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9 19453224 RIKENE FULL | GA7 bp mixth linear EST 13-DEC-2002 BP453224 MISS BP453224. G1:8574220 MISS BP453224.1 G1:8574220 MISS BP453224 MISS BP45322 MISS BP453224 MI
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Barell; Oxford University Press, 1999)."
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High quality sequence start: 13
High quality sequence stop: 783.
Location/Qualifiers
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AZ687690/c
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/db_xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Entamoeba histolytica Stering of Connection of Connectical Approach, eds. M. Vaudin and B.
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                 /tissue_type="whole body"
/dev.stage="13 days embryo"
/clone lib="RIKEN full-length enriched, 13 days embryo
whole body.
mouse tissues.
visit our web site (http://genome.gsc.riken.go.jp) for
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    /organism="Entamoeba histolytica"

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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                               organism="Mus musculus"
/mol type="mRNA"
/strain=CSTBL/6J"
/db xref="taxon:10090"
/clone="K630067H12"
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High quality sequence stop: 855.
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Seq primer: M13-Forward
Class: shotgun
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Matches 36; Conservative
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Entangoeba histolytica
Entangoeba histolytica
Eukaryota; Entangoebidae; Entamoeba.

E 1 (Dasas 1 to 865)

S Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
Uppublished (2000)

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Department of Eukaryotic Genomics
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Tel: 301 838 0208
Fax: 301 838 433
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library AZ687690 865 bp DNA linear GSS 14-DEC-2000 ENTJL91TR Entamoeba histolytica Sheared DNA Entamoeba histolytica ö (Making small insert libraries for H.O. and Venter, J.C. (Making small insert libraries whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barall, Oxford University Press, 1999)." Gaps Gaps 261 TATTAACTCTACAAAAAAAGAAGTAGAACATAAAAAAGGAAAGTTACAAGA 311 ö 59 9 TATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59 9 TATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA Length 858; Match 45.0%; Score 27; DB 28; Length 865; Local Similarity 70.6%; Pred. No. 1.4e+02; les 36; Conservative 0; Mismatches 15; Indels Query Match
45.0%; Score 27; DB 28; Length 85
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Matches 36; Conservative 0; Mismatches 15; Indels /organism="Entamoeba histolytica" /mol_type="genomic DNA" /strain="HM1:IMSS"

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Direct Submission
Submitted (12-ARR-2000) Genoscope - Centre National de Sequencage :
BP 1910 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
          CNS032B1 B91 bp DNA linear GSS 01-SEP-2000 Terraodon nigroviridis genome survey sequence PUC-Ori end of clone 206J09 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                   AL224614
AL224614.1 GI:7883483
ASI224614.1 GI:7883483
GSS, genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha, Acanthopterygii; Percomorpha, Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Aleracterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Brimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
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(db xref="taxon:99883"
/clone="206J09"
/clone="206J09"
/clone lib="Genoscope sequence ID : COAG206CE05SP1-end PUC-Ori"
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44.3%; Score 26.6; DB 29; Length 891;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0
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AUTHORS
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AUTHORS
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JOURNAL
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3, 2004, 00:54:00 Search completed: June Job time: 1505.5 secs us-10-069-056-3.rni

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HYPOTHETICAL:
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-647-655-1
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US-09-543-681A-2411
US-08-961-527-15
US-09-543-681A-3781
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US-09-439-313-440
US-09-55-616A-440
US-09-685-166A-440
US-08-685-166A-440
US-08-685-170A-41
US-08-692-787-47
US-08-677-010-1
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US-08-777-010-1
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US-09-543-681A-2540
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Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
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Patent No. 5814510
GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland B.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.6; DB 1; Length 5049;
Pred. No. 0.28;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FLING DATE:
                      US-09-221-107-54
US-09-833-381-496
US-09-543-6818-496
US-09-306-446C-1
US-09-543-6818-2681
US-08-545-528D-1
US-09-107-532R-1083
US-09-107-532R-1083
US-09-108-192R-142
US-09-128-352-3053
US-09-128-352-3053
US-09-128-352-2606
                                                                                                                                                                                                                                 US-09-016-434-1096
US-09-023-655-955
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US-09-615-192A-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8664/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER.STICS:
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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67.8%;
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Best Local Similarity 67.8
Matches 40; Conservative
                     494
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951
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1032
580073
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COMPUTER READABLE FORM:
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ORGANISM: Par
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
ORGANISM: Parvovirus
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US-08-647-655-2
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                              1116 GAAGTGTCAATCAAATGTACTTTGCGGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
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| Sequence 1, Application US/08647655
| Parent No. 58853185
| GENERAL INFORMATION:
| APPLICANT: Parrish, Colin R. APPLICANT: Carmicherg, Allen
| APPLICANT: Gruenberg, Allen
| APPLICANT: Gruenberg, Allen
| APPLICANT: Gruenberg, Allen
| APPLICANT: Gruenberg, Allen
| APPLICANT: Carmicherg, Altenuated Canine Parvovirus Vaccine
| ITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Pennie & Edmonds
| STREET: 1155 Avenue of the Americas
| CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%; Score 28.6; DB 1; Length 5049; 67.8%; Pred. No. 0.28;
                                                                                                                                                                                                                                        APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
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NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 86-9864/9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5049 base pairs
                                                                                                                                                               Sequence 2, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 67.8
Matches 40; Conservative
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US-08-336-345-2
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
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STATE: New York
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COMPETER IN THE COMMENTAGE #1.0, Version #1.25

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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 TIGCTCTTAAAACTCAACNCCTGTTGCAAGTTCATACAAGTGTTACCCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCAC 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
CCMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: PCT/GB94/00846
FILING DATE: 02-MAY-1994
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
US/08/737,109
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IMMEDIATE SOURCE:
LIBRARY: lambda FixII type
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; Sequence 15, Application US/08961527
; Patent No. 6420135
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P834(
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFRA: (301) 309-8512
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                     LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.73
Matches 34; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CLASSIFICATION: 424
APPLICATION NUMBER:
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US-08-737-109-13
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LEMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                         1116 GAAGTGTCAATCAAATGTACTTTGCGGACTTGGTTAGTAAAAGAGTAACATCACCTGA 1174
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APPLICANT: ELBOROUGH, Kierzan Michael
APPLICANT: ERBOROUGH, Kierzan Michael
APPLICANT: ERTGHT, Simon William Jonathan
APPLICANT: FENTEM, Philip Anthony
TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A
TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                          1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 AGTTGTCGATAAAACAACCAATAAAGAGCTTGCTCATTACAAATTAACGGAACAAG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AGTIGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAG 58
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0
                                                                                                                                                                                                                                                             Score 28.6; DB 2; Length 5049;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.7%; Score 25.6; DB 4; Length 597; 66.1%; Pred. No. 2; ive 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08737109
Patent No. 6455688
GENERAL INFORMATION:
                                                                  TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.8%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.7%;
Best Local Similarity 66.1%;
Matches 37; Conservative
5049 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Proteus mirabilis
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                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-543-681A-2411
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US-08-737-109-13/c
                                                                                                                                                                                                                US-08-647-655-2
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                                                                                                                                                                                                                                                                                                                                                ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (98239). (98239)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (98266). (98266)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (103998)...(103998)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (148948)...(148948)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
JTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
LOCATION: (103598)..(10398)
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (84773)...(84773)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (84808)...(84808)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (18822) .. (2822)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (28257) .. (28258)
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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LOCATION: (98120)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
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                                                                                                                                                                                                                                                                                                  LENGTH: 1664976
                                                                                                                                                                                                                                                                           SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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US-09-543-681A, Application US/09543681A

Sequence 3781, Application US/09543681A

Sequence 3781, Application US/09543681A

Patent No. 6605709

GENERAL INCORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT PILING DATE: 199-04-09

PRIOR PRIOR PILING DATE: 199-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 3781

LENGTH: 213
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 3704
LENGTH: 336
                                                                                                                                                                   7045 AAGAAACTATTAAAGCTGCACTTGTGGAGTTTTTTAATGGAAAAGTCACTTTAACTGA 7102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAGTIGCTATTAAAACTACACTTAAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGA 59
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                                                                                                                          59
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                         DB 4; Length 10993;
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                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23.8; DB 4;
Pred. No. 7.2;
0; Mismatches 22;
                    40.7%; Score 24.4; Dilarity 63.8%; Pred. No. 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
18-09-543-681A-3704/c
18-09-640-0-6 3704, Application US/09543681A
19 Patent No. 6605709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.7%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.77
Matches 37; Conservative
Query Match
Best Local Similarity 6
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US-08-916-421B-1
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
FILE REFERENT APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ 1D NOS: 3
SOFTWARE: Patentin version 3.1
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OTHER INFORMATION: n equals a,
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or g ö or ö ö or or ö or or ör ö or ö οz MAME/KEY: misc feature LOCATION: (319226)..(319226) OTHER INPORMATION: n equals a, t, c, NAME/KEY: misc feature LOCATION: (559167)..(559167) OTHER INFORMATION: n equals a, t, c, ບັ υÌ NAME/KEY: misc_feature
LOCATION: (1096846)...(1096846)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1119881)...(1119881)
OTHER INFORMATION: n equals a, t, AME/KEY: misc feature OCATION: (657203)..(657203) THER INFORMATION: n equals a, t, ANE/KEY: misc feature COCATION: (779676)..(779676) THER INFORMATION: n equals a, t, AME/KEY: misc feature OCATION: (855539)..(855539) THER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (1130881)..(1130881) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (622708)...(622708) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (657081)...(657081) OTHER INFORMATION: n equals a, t, THER INFORMATION: n equals a, t, ú NAME/KEY: misc feature LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, AME/KEY: misc feature OCATION: (674435)..(674435) MHER INFORMATION: n equals a, TAME/KEY: misc feature OCATION: (741684)..(741684) THER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (1313224)..(1313224) AME/KEY: misc feature LOCATION: (682442)..(682442) JTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (713652)..(713652) JTHER INFORMATION: n equals a, WAME/KEY: misc feature COCATION: (871619)..(871619) THER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (309418) .. (309418) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (312837)..(312837) OTHER INFORMATION: n equals a, LOCATION: (312993)..(312993) OTHER INFORMATION: n equals a, OCATION: (779455)..(779455) THER INFORMATION: n equals a, OCATION: (1084830) .. (1084830) THER INFORMATION: n equals a, NAME/KEY: misc_feature 'KEY: misc_feature NAME/KEY: misc_feature

Gaps Gaps DB 4; Length 1664976; ; 0 ö 39.0%; Score 23.4; DB 4; Length 5428; 67.3%; Pred. No. 22; tive 0; Mismatches 16; Indels 0 405931 AGTTGAATTTAAAGGAACAATTAGAGAGCTGTTAGATAAAGGA 405973 Indels 3 AGTIGCTATIAAAACTACACTIAAAGAGCTGGTGCATAAAAGA 45 APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
CURRENT REPERENCE: MBI-010
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER RILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 119
LENGTH: 5428 12; Query Match 39.7%; Score 23.8; E Best Local Similarity 72.1%; Pred. No. 59; Matches 31; Conservative 0; Mismatches NAME/KEX: misc feature
| IOCATION: (1603734)...(1603734)
| OTHER INFORMATION: n equals a, t, c, or g
| NAME/KEX: misc feature
| IOCATION: (1637998)...(1637998)
| OTHER INFORMATION: n equals a, t, c, or g
| NAME/KEX: misc feature
| IOCATION: (1664854)...(1664855)
| OTHER INFORMATION: n equals a, t, c, or g
| US-08-916-4218-1 b ö or ö ö ö ö ϋ Sequence 119, Application US/09533029 Patent No. 6664446 GENERAL INFORMATION: NAME/KEY: misc feature
LOCATION: (1349473). (1349473)
CTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349491). (1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (147091). (1470091)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1569020)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1602912). (1602912)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t, APPLICANT: Heard, Jacqueline APPLICANT: Broun, Pierre APPLICANT: Ricchmann, Jose-Luis APPLICANT: Keddis, James APPLICANT: Pineda, Omaira TYPE: DNA ORGANISM: Arabidopsis thaliana OTHER INFORMATION: n equals a, Best Local Similarity 67.3 Matches 33; Conservative FEATURE: CTHER INFORMATION: G374 US-09-533-029-119 US-09-533-029-119 Query Match g ઠે

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499 ATTIGCTATGATATATATACTICAAGAGCTGCTATATGTATTACATACATACA 448
3 AGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACTCA 54
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CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT PILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FeatsEQ for Windows Version 3.0
LENGTH: 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.2; DB 4; Length 523; Pred. No. 15; 0; Mismatches 18; Indels
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CURRENT APPLICATION NUMBER: US/09/685,166A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-09-685-166A-440/c
Sequence 440, Application US/09685166A
Patent No. 6630305
                                                                                                                                                                  Sequence 440, Application US/09636215
Patent No. 6620922
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jiang, Yuqui
Henderson, Robert A.
Calos, Michael D.
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Kalos, Michael D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Skeiky, Yasir A.W.
Hepler, William
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Best Local Similarity 65.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                               Mitcham, Jennifer
Harlocker, Susan I
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Vedvick, Thomas (
Carter, Darrick
                                                                                                                                                                                                                                                                            Xu, Jiangchun
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-636-215-440
                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang, Yuqui
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Xi, Jiangchun
APPLICANT:
                                                                                                                 1328 gadararcrarrancescencras and 1376 sadarana 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : COMPOSITIONS AND METHODS FOR THERAPY AND : DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.2; DB 4; Length 52
Pred. No. 15;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CIPILE REFERENCE: 21011.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT PILLIOR DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FREESEQ FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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US-09-352-616A-440/c.
; Sequence 440, Application US/09352616A
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, Jiangchun C. APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan Louise APPLICANT: Harlocker, Susan Louise APPLICANT: Reed, Steven G. APPLICANT: Reed, Steven G. APPLICANT: Kalos, Michael
                                                                                                                                                                                                                                                                                   Sequence 440, Application US/09439313
Patent No. 6329505
                                                        GAAGTTGCTATTAAAACTACACT
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Best Local Similarity 65.4%;
Matches 34; Conservative (
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-09-439-313-440
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Best Local Similarity
Matches 34; Conserv
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US-09-439-313-440/c
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LENGTH: 523
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LENGTH: 523
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Gaps

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; CURRENT FILING DATE: 2000-10-10; NUMBER OF SEQ ID NOS: 898; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 440; ENGTH: 523; TYRE: DNA; TYRE: DNA; TYRE: DNA; TYRE: DNA; OWENY MATCH

QUETY MATCH

Query Match

Best Local Similarity 65.4%; Pred. No. 15; Matches 34; Conservative 0; Mismatchés 18; Indels 0; Gaps 0;
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Search completed: June 3, 2004, 00:56:17 Job time: 36.75 secs

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2, 2004, 23:14:04; Search time 141 Seconds (without alignments) 1941.275 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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60
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	15566,	75051,	56680,	75051,	3694,	3694,	230058	230058	2616, A	154079	154080	154079	154080,
Description	Sequence 15566,	Sequence	Sequence	Sequence	Sequence 3694	Sequence 3694	Sequence 230058	Sequence 230058	Sequence 2616, Ap	Sequence 154079	Sequence 154080	Sequence 154079,	Sequence
SUMMARIES	US-10-282-122A-15566	US-10-027-632-56680 US-10-027-632-75051	US-10-027-632-56680	US-10-027-632-75051	US-10-027-632-3694	US-10-027-632-3694	US-10-027-632-230058	US-10-027-632-230058	US-09-880-107-2616	US-10-027-632-154079	US-10-027-632-154080	US-10-027-632-154079	US-10-027-632-154080
DB	ដូរ	13 13	16	16	13	16	13	16	0	13	13	16	16
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% Query Match	43.7	43.0	43.0	43.0	43.0	43.0	42.7	42.7	42.3	41.7	41.7	41.7	41.7
Score	26.2	25.8	25.8	25.8	25.8	25.8	25.6	25.6	25.4	25	25	25	25
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24.6	11.0	2940 2940	13	US-10-027-632-111618 US-10-027-632-111618	Seguence 111618, Seguence 111618,
	40.7	,	6	US-09-983-965-61	Sequence 61, Appl
	40.7		13	US-10-158-844-15	Sequence 15, Appl
	40.4	1260	7 5	US-UY-YY/-/ZZ-85 US-10-425-114-10451	Sequence 85, Appl Sequence 10451, A
			13	US-10-424-599-54636	
	40.3	80	15	US-10-311-455-768	
₹.	0.0		13	US-10-424-599-40801	4080
24 4(0.	446	10	US-09-918-995-23611	Sequence 23611, A
4	0.		13	US-10-027-632-40376	Seguence 40376, A
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4	40.0	1012	16	US-10-027-632-100959	Sequence 100959,
24 40	٥.		19	US-10-027-632-100960	
4	40.0		13	US-10-221-278-489	Sequence 489, App
4.	40.0	•	16	US-10-291-172-489	-
4.	0.		13	US-10-282-122A-11029	
	0.	107	13	US-10-087-192-361	
			13	US-10-424-599-84615	8461
23.8 35	.7	33	12	US-09-997-722-109	
		322	13	US-10-027-632-14611	1461
	9.3		16	US-10-027-632-14611	
	9.3		13	US-10-027-632-221768	Sequence 221768,
	39.3		16	US-10-027-632-221768	Sequence 221768,
	9.3	-	13	US-10-027-632-130629	Sequence 130629,
23.6 3	9.3	603	16	US-10-027-632-130629	Sequence 130629,

ALIGNMENTS

US-10-282-122A-15566

PUBLICATION NO. US20040029129A1

GENERAL INFORMATION:

APPLICANT WANG, Liangeu

APPLICANT Wand, Liangeu

APPLICANT Wand, Liangeu

APPLICANT Wand, Liangeu

APPLICANT Wand, Wari

APPLICANT Wand, Wari

APPLICANT Wand, Wari

APPLICANT Wand, Wari

APPLICANT Wand, Wal, Daniel

APPLICANT Carr, Grart

APPLICANT Carr, Grart

APPLICANT Wand, Wand, Wand

APPLICANT Carr, Grart

APPLICANT Wand, Wand

APPLICANT Carr, Grart

APPLICANT

PRIOR APPLICATION NUMBER: 60/230, 335

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-01-03

PRIOR PILIN

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5 TTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA
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0; Mismatches
                                                PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
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Best Local Similarity 73.3
Matches 33; Conservative
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US-10-027-632-56680/c
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ORGANISM: Human
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1091 Aagaagragrrahaaaracacrraaagagcrrgrraaaaarggaara 1137
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Pred. No. 44;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAGTIGCTAITAAAACTACACTIAAAAGAGCIGCTGGTGCATAAAAGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26.2; |
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILLE OF INVALIDOR: POLYMOLPHISMS IN LHE FIRE
FILE REPERRICE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PELLING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56680, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75051, Application US/10027632
Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-15566
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.3%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%;
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Best Local Similarity 73.3
Matches 33; Conservative
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US-10-027-632-75051/c
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US-10-027-632-56680
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LENGTH: 502
                                                                                                                                                                                                                                  SEQ ID NO 15566
LENGTH: 2931
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DB 13; Length 502;

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
PILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLING DATE: 2000-07-12
PRIOR PLLING DATE: 2000-07-12
PRIOR PLLING DATE: 2000-04-20
PRIOR PLLING DATE: 2000-04-20
PRIOR PLLING DATE: 2000-03-24
PRIOR PLLING DATE: 2000-03-24
PRIOR PLLING DATE: 1999-11-23
PRIOR PLLING DATE: 1999-11-23
PRIOR PLLING DATE: 1999-10-24
PRIOR PLLING DATE: 1999-10-24
PRIOR PLLING DATE: 1999-09-28
PRIOR PLLING DATE: 1999-09-28
PRIOR PLLING DATE: 1999-09-09
PRIOR PLLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
PRIOR PLINGS: 325720
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190 irraicitraagraacriraaagagargerecaraagaaa 146
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Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                         Sequence 56680, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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73.3%;
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Best Local Similarity 73.39
Matches 33; Conservative
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

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Gaps

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US-IU-V6/-056-3804, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANTY Wang, David G.

TITLE OF INVENTION: IGENTIFICATION and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PRIOR PRILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-02-24

PRIOR PRILING DATE: 2000-02-24

PRIOR PRILING DATE: 2000-02-24

PRIOR PRILING DATE: 2000-03-29

PRIOR PRILING DATE: 2000-03-29

PRIOR PRILING DATE: 2000-03-29

PRIOR PRILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3694
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Publication No. US20020198371A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE SPERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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                                                                                                                                                                                                                                                             DB 13; Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 TTTATCTTTAAAGTAACTTTAAAGAGATGGTGCATAACAAAGAAA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 ritraictitraagtaactitraaagagatggtgcataacaaagaa 497
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                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                      Score 25.8; DB Fred. No. 48; Ob Mismatches
; TYPE: DNA; Human; ORCANISM: Human; PEATURE:
; NAME/KEY: misc_feature; LOCATION: (1)...(672); OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 73.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-027-632-3694
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                                                                                                            US-LUCATOR ADDITIONAL TO SEQUENCE 75051, Application US/10027632

PUBLICATION NO. US2003020407549

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

FRIOR APPLICATION NUMBER: US 60/198,676

FRIOR PELING DATE: 2000-07-20

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-03-29

FRIOR PELING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-02-24

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-10-08-09

FRIOR FILING DATE: 1999-10-08-09

FRIOR FILING DATE: 1999-09-08-09

FRIOR FILING DATE: 1999-09-08-09

FRIOR FILING DATE: 1999-08-09

FRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25.8;
Pred. No. 44
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PRIOR PELICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/165,218
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-33
PRIOR PILING DATE: 1999-10-38
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3694, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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Best Local Similarity 73.3.
Best Local 33; Conservative
                                                                 RESULT 5
US-10-027-632-75051/c
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US-10-027-632-75051
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; ORGANISM: Human
US-10-027-632-154079
                                                                                     -09-880-107-2616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AAATTTCAAGTAAATTTTTCATTTGAAAACTCTTGCTTAAAACAATAWCAACAACAAA 72
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Bublication No. US2003020407549

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108027.129

FUCREENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR PELIOR NUMBER: US 60/165,358

PRIOR PELIOR UNMBER: US 60/166,358

PRIOR PELIOR DATE: 1999-09-28

PRIOR PELIOR DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-00-28
PRIOR FILING DATE: 1999-00-28
PRIOR FILING DATE: 1999-00-28
PRIOR FILING DATE: 1999-00-3
PRIOR FILING DATE: 1999-00-3
PRIOR FILING DATE: 1999-00-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRASESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.84
Them 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.8
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 230058
LENGTH: 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 230058
LENGTH: 597
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Gaps

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Deblymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/010/027,632
CURRENT APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-08-09
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 GAAATTAATAAGCCATCCATAGTTAAAGAGCTAGTGAATGACAGAGTAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA 49
                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 925;
1e+02;
ches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 16;
Pred. No. 1e+02;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 1
Pred. No. 1e+02
0; Mismatches
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154079
LENOTH: 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 154080, Application US/10027632; Publication No. US20030204075A9
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                                                                                                                                                                                                                                                                                                                                                             41.78;
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Best Local Similarity 69.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.4°
Matches 34; Conservative
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US-10-027-632-154080
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US-10-027-632-154080
                                                                                                                                                                                                                                                                          US-10-027-632-154079
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITTLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US 60/218,006
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1900-02-44
FRIOR FILING DATE: 1900-02-44
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-08
FRIOR F
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-24
PRIOR PILING DATE: 1999-09-28
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                                                                                                     493 GAAATTAATAAGCCATCCATAGTTAAAGAGCTAGTGAATGACAGAGTAA 541
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                                                       1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCTAAAAGAGTAA 49
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                                                                                                                                                                                                                                                                                                                                                             , Sequence 154080, Application US/10027632; Publication No. US20020198371A1
                                                                                                                                                                                                                                                                          RESULT 12
US-10-027-632-154080
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US-10-027-632-154080
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: A Covalic David K
APPLICANT: A Covalic David K
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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                                                                         Gaps
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                                                                                                                                                                                                       493 GAATTAATAAGCCATCCATAGTTAAAGAGCTAGTGAATGACAGAGTAA 541
Length 925;
                                                                                                                                           1 GAAGTTGCTATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAA
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56717
; LENGTH: 1844
; TYPE: DNA
; PEATURE:
; CRGANISM: Glycine max
; FEATURE:
; O'HER INPORMATION: Clone ID: PAT_MRT3847_22226C.1
US-10-424-599-56717

QUETY MATCH
Best Local Similarity 67.3%; Pred. No. 1.5e+02;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps
QY
QY
9 TATTAAAACTACACTTAAAGAGCTGGTGCATAAAAGAGTAACCTCACCAGAG 60
Db 978 TATTAAAACTTACAGACATGATTAAAGAGAGAGAGAGACCCAAAG 1029
Search completed: June 3, 2004, 03:14:05
Job time: 142 secs
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(without alignments)
118.967 Million cell updates/sec
                                                                                                                                                                     May 28, 2004, 12:48:18 ; Search time 47.5 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                 OM protein - protein search, using sw model
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1586107 seqs, 282547505 residues 1 EVAIKTTLKELVHKRVTSPE 20 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-069-056-5 97 Scoring table: score: Sequence: Searched: Perfect

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% .Maximum Match 100%

geneseq11980s:*
geneseq11990s:*
geneseq12000s:*
geneseq12001s:*
geneseq12001s:*
geneseq12001s:*
geneseq12001s:* A_Geneseq_29Jan04:* 1: genesecn1980e.* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ion	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Sequence	Novel hum	Talin C-t	Enterohae	Human pre	Human pre		Human ORF	Human Tal	Breast ca	Rat Prote	Human Pro	Rat Prote	Human Pro	Protein's	Human pro	Human pol	Human pol	Human str
Description	Aay72703	Aay72704	Aay72708	Aay72710	Aay72706	Aay72702	Aap40306	Abg03712	Aar76871	Adc01077	Abg70144	Abg70135	Aaw85601	Aab41087	Abb81459	Abr47614	Ade58866	Add45522	Add45520	Ade58868	Abr53759	Aam79794	Aam41079	Aam41098	Aae33668
													•												
ΩI	AAY72703	AAY72704	AAY72708	AAY72710	AAY72706	AAY72702	AAP40306	ABG03712	AAR76871	ADC01077	ABG70144	ABG70135	AAW85601	AAB41087	ABB81459	ABR47614	ADE58866	ADD45522	ADD45520	ADE58868	ABR53759	AAM79794	AAM41079	AAM41098	AAE33668
DB	4	4	4	4	4	4	~1	4	7	7	ហ	Ŋ	7	m	2	9	7	7	7	7	9	4	4	4	9
* Query Match Length DB	20	672	672	672	672	672	069	674	200	250	548	698	777	2541	2541	2541	2541	2541	2541	2541	166	1177	1177	1177	2542
% Query Match	100.0	100.0	6.96	6.96	6.96	96.9	59.8	47.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	45.4	45.4	45.4	45.4	45.4
Score	97	97	94	94	94	94	28	46	45	45	45	45	45	45	45	45	45	45	45	45	44	44	44	44	44
Result No.	п	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu65078 Human NOV	Aay77815 Yeast Sen	Abw01202 Saccharom	Aag31112 Arabidops	Aag31111 Arabidops	Aag31110 Arabidops	_	Abu25772 Protein e	Abul1579 Human MDD	Abg11447 Novel hum	Aao21805 Lung-spec	Aag00595 Human sec	Aab93292 Human pro	Abp62932 Human pol	Abg31585 Human L-i	Adb09803 Alloiococ	Aaw31628 Aspergill	Abr41168 Human DIT	Aao12652 Human pol	Abr40559 Human sec
ABU65078	AAY77815	ABW01202	AAG31112	AAG31111	AAG31110	ABR53451	ABU25772	ABU11579	ABG11447	AA021805	AAG00595	AAB93292	ABP62932	ABG31585	ADB09803	AAW31628	ABR41168	AA012652	ABR40559
S	m	7	m	ო	ო	9	9	9	4	Ŋ	ო	4	ß	Ŋ	9	7	9	4	Ŋ
2545	471	472	1034	1069	1121	2000	66	431	1005	99	91	361	361	361	378	397	413	112	160
45.4	44.8	44.8	44.8	44.8	44.8	44.8	44.3	44.3	44.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3	42.8	42.3
44	43.5	43.5	43.5	43.5	43.5	43.5	43	43	43	42	42	42	42	42	42	42	42	41.5	41
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

/note= "Wild type Ser substituted with Ala; This location corresponds to position 283 of the NS1 variant (S283A) shown in AAY72704" NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant. Parvovirus non-structure protein 1 (NS1) variant (S283A) peptide. Location/Qualifiers AAY72703 standard; peptide; 20 AA. (first entry) (revised) Key Misc-difference 06-AUG-2003 31-MAY-2001 Parvovirus Synthetic AAY72703;

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. 99EP-00115161. 99EP-00115161 EP1077260-A1. 13-AUG-1999; 13-AUG-1999; 21-FEB-2001.

Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

Rommelaere J;

Nueesch J,

WPI; 2001-212717/22. N-PSDB; AAD02798.

Disclosure; Page 14; 41pp; English.

The present sequence is a peptide fragment of parvovirus non-structure protein I (NS1) variant (\$283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the

AAY72708 standard; protein; 672 AA.

RESULT 3

281 EVAIKTTLKELVHKRVTSPE 300

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The present sequence is parvovirus non-structure protein 1 (NS1) variant (S283A). The invention relates to the variants of the parvovirus nonstructure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
cytotoxicity activity. These variants are useful as toxins for treating
                                                                                                                                                                                                                                                                                                                                                                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                         Gaps
           tumoural diseases. The variant DNAs are useful as vectors for genetherapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                       100.0%; Score 97; DB 4; Length 20; 100.0%; Pred. No. 2.4e-09;
                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Parvovirus non-structure protein 1 (NS1) variant (S283A)
                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 14-16; 41pp; English.
                                                                                                                                                                                                                                                               AAY72704 standard; protein; 672 AA.
                                                                                                                                                    EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                  EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-00115161.
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                                                                                       Query Match
Best Local Similarity 100.
Matches 20; Conservative
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N-PSDB; AAD02799.
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Best Local Similarity
Matches 20; Conserv
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Misc-difference
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                                                            Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (T394A). The invention relates to the variants of the parvovirus nonstructure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is parvovirus non-structure protein 1 (NS1) variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                        NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                         /note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.9%; Score 94; DB 4; Length 672;
95.0%; Pred. No. 4.8e-07;
ive 1; Mismatches 0; Indels
                                                                                              Parvovirus non-structure protein 1 (NS1) variant (T394A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 25-27; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72710 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                            99EP-00115161.
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(first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Nueesch J, Rommelaere J;
                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-212717/22.
                                                                                                                                                                                                                            Misc-difference 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD02803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                            13-AUG-1999;
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31-MAY-2001
                                                       06-AUG-2003
                                                                                                                                                                                                                                                                                                 21-FEB-2001
                                                                                                                                                                      Parvovirus
                                                                                                                                                                                    Synthetic.
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                           AAY72708;
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Gaps

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0; Indels

0; Mismatches

Conservative

1 EVAIKTILKELVHKRVTSPE 20

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The present sequence is parvovirus non-structure protein 1 (NS1) variant (T363A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                      Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parvovirus wild-type non-structure protein 1 (NS1).
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 4; Le:
Pred. No. 4.8e-07;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                          (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY72702 standard; protein; 672 AA.
                                                                                                                                                                                                                                                              Claim 6; Page 19-21; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 EVSIKTTLKELVHKRVTSPE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumoural disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                             96.98;
                                                    99EP-00115161
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(first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rommelaere J;
                                                                                                                                     Rommelaere
                                                                                                                                                                2001-212717/22.
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N-PSDB; AAD02797.
                                                                                                                                                                             N-PSDB; AAD02801
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 672 AA;
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EP1077260-A1
                                                     13-AUG-1999;
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31-MAY-2001
                          21-FEB-2001
                                                                                                                                     Nueesch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nueesch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY72702;
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AAY72702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (T463A). The invention relates to the variants of the parvovirus non-
structure protein (NS1) having a shifted equilibrium between the DNA
replication and transcription activities, and the cytotoxicity activity.
These variants are useful as toxins for treating tumoural diseases. The
variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is parvovirus non-structure protein 1 (NS1) variant
                                                                                                                                                                                                                                                                                                                                                                       Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                        NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                    /note= "Wild type Thr substituted with Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 672;
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Parvovirus non-structure protein 1 (NS1) variant (T463A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parvovirus non-structure protein 1 (NS1) variant (T363A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94; DB 4; I
Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 30-32; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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95.0%;
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                                                                                                                                                                                                                                                                                                      Nueesch J, Rommelaere J;
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                 2001-212717/22
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD02805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 672 AA;
                                                                                                                       Misc-difference
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                                                                                                                                                                EP1077260-A1
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31-MAY-2001
                                                                  Parvovirus.
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                                                                                Synthetic
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Gaps

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4; Length 672; Indels Ą

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #3703
                             282 EVSIKCTIRDLVNKRCTSIE 301
  1 EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                    ABG03712 standard; protein; 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity
                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001
                                                                                                                                                                                                                      ABG03712;
                                                                                                                     ABG03712
                                            용
                                                                                                                                                                                             The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoded by the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                    96.9%; Score 94; DB 4; Length 672; 95.0%; Pred. No. 4.8e-07; Live 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein envelope; immunogen; vaccine; antigen; epitope.
transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP40306 standard; protein; 690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVAIKTTLKELVHKRVTSPE 20
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84US-00567968
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Best Local Similarity 60.0
Matches 12, Conservative
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Matches 19; Conserv
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12-JAN-1992
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Tang YT;

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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic and amino acid sequences.
                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Claim 20; SEQ ID NO 34071; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KTTLKELVHKRVTSPE 20
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Best Local Similarity 56.2*
Local Similarity 56.2*
Part of the conservative
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0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection has and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterchaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel enterohaemorragic Escherichia coli
                                                                                                                                                        Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 7; Length 250;
Pred. No. 31;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 1121; 2067pp; Japanese.
                     ADC01077 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG70144 standard; protein; 548 AA
                                                                                                                                                                                                     enterohaemorragic; anti-bacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%;
                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2002; 2002JP-00015959
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2001; 2001JP-00112010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ||: :|| :| |
183 TLLKDFIHKHITRP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TTLKELVHKRVTSP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-2002 (first entry)
                                                                                                              (first entry)
                                                                                                                                                                                                                                                 Sacherichia coli; 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.4
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYTS-) UNIV TSUKUBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-451640/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 250 AA;
                                                                                                                                                                                                                                                                                              JP2002355074-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                              04-DEC-2003
                                                                                                                                                                                                                                                                                                                                          10-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG70144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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ADC01077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Talin binds to vinculin and this is reduced on incubation with, e.g. Vinl Talin binds to vinculin and this is reduced on incubation with, e.g. Vinl Talin binds to vinculin and this is reduced on incubation with, e.g. Vinl 2.1. Vinl2.1 is a specific vinculin binding peptide generated from a TSAR (Totally Synthetic Affinity Reagent) 12 library. Many changes at the Neternatus are not disruptive whereas most changes at the C-terminus are disruptive. Mutagenesis of Vinl2.1 was carried out deliberately contaminating the precursor reservoirs used to construct the contaminating the precursor reservoirs used to construct the vinculin binding TSARs may alter the mobility or attachability of malignant cells, binding TSARs may alter the mobility or attachability of malignant cells, perhaps preventing or inhibiting metastaels. The TSARs are new and/or improved heterofunctional binding fusion proteins that have affinity for the ligand vinculin, and can be used to modulate the activity of the pharmaceuticals, etc. Other TSARs can be designed to bind dynein and glutathione-S-transferase. Typical applications are: (i) inhibition of GST to treat cancers that produce high levels of this enzyme; (ii) attenting mobility/attachment of malignant cells, modulating platelet release and blood clotting, for TSARs directed against vinculin; (iii) TSARs against dynein are used to modulate nerve cell activity, sperm motility, mobility of protozoa, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying peptide(s) that bind specifically to dynein, vinculin or enzymes, eg. glutathione-S-transferase - by screening random peptide libraries, useful e.g. in immunoassays, affinity purification., tumour treatment, etc.
                                                                                                                                                                                                                                                                                           totally synthetic affinity reagent; vinculin; dynein; enzyme; heterobifunctional binding fusion protein; glutathione S-transferase; cancer treatment; nerve cell activity; modulate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.4%; Score 45; DB 2; Length 200;
55.6%; Pred. No. 24;
iive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7.2.4; Page 65; 110pp; English.
                                                                                                                AAR76871 standard; peptide; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AIAVTVQEMVTKSNTSPE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AIKTTLKELVHKRVTSPE 20
  382 RTCLKDSVHQRVSSAE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparks AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US001286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00189331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                 Falin C-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-275411/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adey NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 200 AA;
                                                                                                                                                                                                     08-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9520601-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                        AAR76871;
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Kay

AAR 76871 9
AAR 76

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Gaps

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Prey protein; ospB; ospD1; ipaD; ipaH9.8; ospG; ospC1; Shigella; shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system; protein-protein interaction; SID; selected interacting domain; human.
Human prey protein for Shigella ipaC #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2002; 2002WO-EP000777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-2001; 2001US-0261130P.
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Matches

RESULT 10

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Legrain P;

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The invention relates to a complex of protein-protein interactions between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC, ipaH9.84 ospG and ospC1) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the Shigella flexneri polypeptide and a mammalian polypeptide defined in the specification; (2) selecting a modulating compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID (2) (3) a selected interacting domain) polypeptide or its fragment or variant comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a SID polymucleotide or its fragment or variant comprising the above polypeptides a vector comprising (5); (6) a recombinant host cell containing the vector; and (10) a protein chip comprising shigella .

Clexneri polypeptide and a mammalian polypeptide defined in the specification. A pharmaceutical composition comprising the compound, belighted to polypeptide is useful for treating or preventing shigellosis (bacillary dysentery) in a human or mammal. The present sequence represents a human prey protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a shigella protein
                                                                                                             flexneri polypeptide and a prey mammalian or human placenta polypeptide
for treating or preventing bacillary dysentery in a mammal or human.
                                                                                     New complex of protein-protein interactions between a bait Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hexosaminidase; enzyme; laundry; cleaning agent; hydrolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 5; Length 698; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-microbial; detergent; surfactant.
                                                                                                                                                                                                      Claim 7; Page 98-99; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW85601 standard; protein; 777 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US009125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0056132P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hexosaminidase enzyme
  2002-599706/64.
WPI; 2002-599706,
N-PSDB; ABS51528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 698 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                New complex of protein-protein interactions between a bait Shigella flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a complex of protein-protein interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prey protein for Shigella ipaD #12.
                                                                                                                                                                                                                                                                                                                 Claim 7; Page 101-102; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG70135 standard; protein; 698 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2002; 2002WO-EP000777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                             WPI; 2002-599706/64.
N-PSDB; ABS51537.
(HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 548 AA;
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Gaps

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5; Indels

Laundry and cleaning compositions containing hexosaminidase - to provide

Wolff AM;

Convents AC, Moese RL,

12-JAN-2001; 2001US-0261130P.

ABG70135;

RESULT 12

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(HYBR-) HYBRIGENICS

Legrain P;

WPI; 1999-024116/02.

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Claim 11; Page 1357; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
8
                                                                                                                                                                                                                                                                             1;
                                                            enzymes (AAW85599-605) can be used in combination in
                                                                      an aqueous laundry or cleaning product. The cleaning product is used especially used to launder fabrics and to clean dishes and tableware, particularly in an automatic dishwasher, but may also be used generally as hard surface cleaner. The cleaning product imparts antimicrobial activity and/or eliminates biofilm, the hexosaminidases having a minimum inhibitory concentration of less than about 0.125% but more preferably less than about 0.025%. (NB: entry was revised to change incorrect cross references in Comments field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; alleryy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                               Length 777;
                                                                                                                                                                                                                                            46.4%; Score 45; DB 2; Length 777
40.9%; Pred. No. 1.2e+02;
ive 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for treating e.g. cancers, proliferative disorde
neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF851 polypeptide sequence SEQ ID NO:1702.
antimicrobial activity and remove biofilm.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB41087 standard; protein; 2541 AA
                                                                                                                                                                                                                                                                                                                           || ::|:|:|
EVGTVSSLEEIMHGKEKITSPE 673
                              Claim 2; Page 39-40; 64pp; English.
                                                                                                                                                                                                                                                                                                          1 EVAIKTILKELVH--KRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0127607P.
99US-0127636P.
99US-0127728P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 40...
Best Local Similarity 40...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leach M;
                                                            Novel hexosaminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC75296.
                                                                                                                                                                                                                Sequence 777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB41087;
                                                                                                                                                                                                                                                                                                                                          652
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; noctropic; hepatotropic; vulnerary; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressaive; antiinfinamatory; antibacterial; antiviral; antifined sanciamatory; antibacterial; corresponded for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an order therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, cardiovascular disease, disorders neurodegenerative severe disorders, osteoarthritis, antipothyroidism, cholesterol ester charage, systemic lupus erythematosus, severe combined immunodeficiamcy corresponded immunodeficiancy corresponded immunodeficianc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an antisense compound ({\tt I}), 16 to 30 bases in length targeted to specific base regions of a nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Talin, antimicrobial, antiinflammatory, cytostatic, inhibitor; antisense gene therapy, infection, inflammation, Talin inhibitor; tumour; antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound useful for inhibiting expression of Talin and for preventing or delaying infection, inflammation or tumor formation.
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.4%; Score 45; DB 3; Length 254
55.6%; Pred. No. 4.8e+02;
ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Col 43-60; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB81459 standard; protein; 2541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |::|:| | ||||
1863 AIAVTVQEMVTKSNTSPE 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Talin protein SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-2000; 2000US-00702251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-2000; 2000US-00702251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AIKTTLKELVHKRVTSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 55.6
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-470102/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABN89190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2002
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human Talin. Also described: (a) an antisense compound up to 30 bases in length which inhibits the expression of human Talin; (b) a composition [II] comprising [I] or (a); and (c) inhibiting the expression of human Talin in human cells or tissues comprising contacting the cells or tissues in vitro with (I) or (a). (I) has antimicrobial, antinflammatory and cytostatic activities, and can be used in antisense gene therapy and as a Talin expression inhibitor. (I) can be used: to inhibit the expression of human Talin in human cells or tissues; to prevent or delay infection, inflammation or tumour formation; and in diagnostics, the reapentics, prophylaxis, and in research reagents and kits. The present sequence represents human Talin from the present invention
          88888888888888888888
```

Query Match 46.4%; Score 45; DB 5; Length 254 Best Local Similarity 55.6%; Pred. No. 4.8e+02; Matches 10; Conservative 3; Mismatches 5; Indels || |::|:| | |||| 1863 AIAVTVQEMVTKSNTSPE 1880 3 AIKTILKELVHKRVTSPE 20 g ò

Search completed: May 28, 2004, 12:57:02 Job time : 49.5 secs

· 0

0; Gaps

Length 2541;

Sequence 2541 AA;

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May 28, 2004, 12:52:43 ; Search time 10.5 Seconds (without alignments) 183.222 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                               Run on:
```

1 EVAIKTTLKELVHKRVTSPE 20 US-10-069-056-5 97 Perfect score: Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Match Length Score Result No.

Description	noncapsid protein				noncapsid protein					noncapsid protein		hypothetical prote	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat		probable head size	hypothetical prote	talin - mouse	hypothetical prote	hypothetical prote	SEN1 protein - yea	hypothetical prote	hypothetical prote	phosphate starvati	hypothetical prote	hypothetical prote		probable transcrip
ar T	A44276	UYPW1	UYPV1M	UYPVIM	UYPV1F	UYPVCP	UYPVME	UYPVFP	UYPVPP	UYPVNA	B82175	AE2203	S37072	S18318	S25082	AC2401	B90666	E85516	S11661	S64906	T06065	S53416	B64203	B96841	C70417	T26261	D72742	A83904	T38673
e i	-	Н	Н	7	Н	٦	Н	-	٦	ч	~	7	~	~	0	7	~	N	~	N	~	~	П	~	N	7	~	7	7
Match Length DB	899	672	672	721	392	668	668	668	099	662	637	790	996	996	196	207	250	250	2541	166	1121	2231	186	327	348	1023	144	672	1108
Match	6.96	6.96	6.96	6.96	75.3	75.3	75.3	75.3	59.8	59.8	47.4	47.4	47.4	47.4	47.4	46.4	46.4	46.4	46.4	45.4	44.8	44.8	44.3	44.3	44.3	44.3	43.3	43.3	43.3
Score	94	94	94	94	73	73	73	73	58	28	46	46	46	46	46	45	45	45	45	44	43.5	43.5	43	43	43	43	42	42	42
ė.	п	0	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	conserved hypothet	hypothetical prote	Na+/H+ antiporter	phragmoplastin 5 -	hypothetical prote	hypothetical prote	neural specific DN	molybdopterin bios	hypothetical prote	probable upp prote	hypothetical prote	hypothetical prote	IMP dehydrogenase	hypothetical prote	excinuclease ABC c
T08026	D69430	T21977	G82125	563668	T45726	T00075	T30884	AH3489	AC3405	D70842	873123	S56224	AG0349	S73547	F69157
~	~	~	~	~	7	~	~	7	~	7	0	0	N	-	7
2971	495	361	481	610	951	1355	1361	321	139	207	238	385	487	561	579
43.3	42.8	42.3	42.3	42.3	42.3	42.3	42.3	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2
	2	41	41	41	41	41	41	10.5	40	40	40	40	40	40	40
42	41.							•							

ALIGNMENTS

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Cispecies: parvovirus LuIII
Cispecies: parvovirus LuIII and localization of a uniquate number: A4276
Airtle: The complete nucleotide sequence of parvovirus LuIII and localization of a uniquate number: A44276
Airtle: The complete nucleotide sequence of parvovirus LuIII and localization of a uniquaterence number: A44276
Aircession: A4276
Aircession: A4276
Aircession: A4276
Aircession: A4276
Aircession: parvovirus not shown
Aircession: Diametric Aircession: Cisperfamily: parvovirus noncapsid protein
Cisberfamily: parvovirus noncapsid protein
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Query Match 96.9%; Score 94; DB 1; Length 668; Best Local Similarity 95.0%; Pred. No. 3.6e-07; Matches 19; Conservative 1; Mismatches 0; Indels

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281 EVSIKTTLKELVHKRVTSPE 300 1 EVAIKTTLKELVHKRVTSPE 20 g ઠે

RESULT 2

noncapsid protein NS1 - parvovirus H1 C;Species: parvovirus H1

and mapping of its genes by hybric A.Note: host Homo sapiens (man)
C.Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
C.Accession: A03695
C.Accession: A03695
J. Virol. 45, 173-184, 1983
A.Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hyk A; Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hyk A; Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hyk A; Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hyk A; Title: Parvovirus M03695; MUD: 83112183; PMID: 6823009
A; Accession: A03695
A; Molecule type: DNA
A; Residues: 1-672 < RML
A; Residues: 1-672 < RML
A; Crose-references: EMBL: X01457; NID: g60993; PIDN: CAA25689.1; PID: g60994; EMBL: J02198
C; Superfamily: parvovirus noncapsid protein

ö Score 94; DB 1; Length 672; Pred. No. 3.7e-07; 1; Mismatches 0; Indels 1 EVAIKTTLKELVHKRVTSPE 20 96.98; Query Match
Best Local Similarity 95.03
Matches 19; Conservative ઠે g

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Gaps

281 EVSIKTTLKELVHKRVTSPE 300

Gaps

A; Molecule type: DNA

Query Match

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noncapsid protein NSI - mink enteritis virus (strain Abashiri)
C;Species: mink enteritis virus, MEV
C;Decies: mink enteritis virus, MEV
C;Decies: mink enteritis virus, MEV
C;Decies: mink enteritis virus, MEV
C;Decession: A38350
R;Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinaga, J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the A;Reference number: A38350, MUID:91202123; PMID:2016597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29962
R;Reed, A.P.; Jones, E.V.; Miller, T.J.
J. Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine parvovirus.
A;Reference number: A29962; MUID:88062992; PMID:2824850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            noncapsid protein NS1 - feline panleukopenia virus (strain 193)
C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A36608
A, Residues: 1-392 <CAR.
A, Rossidues: 1-392 <CAR.
A, Cross-references: EMBL.M10824, NID:9333474; PIDN:AAA47160.1; PID:9333475
C, Superfamily: parvovirus noncapsid protein
C, Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:M19296; NID:g333438; PIDN:AAA67459.1; PID:g333439 C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein
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**Residues: 1-668 < KAR>
**Residues: 1-668 < KAR>
**A;Cross-references: GB:D00765; NID:g222435; PIDN:BAA00662.1; PID:g222436
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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0
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                                                                                                                                                                      Score 73; DB 1; Length 392
Pred. No. 0.00053;
3; Mismatches 2; Indels
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Pred. No. 0.00095;
3; Mismatches 2; Indels
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75.0%; Pred. No. 0.00095;
Micmatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noncapsid protein NS1 - canine parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 EVSIKCTLRDLVSKRVTSPE 301
                                                                                                                                                                                                                                                                                                                                             ||:|| ||::|| |||||||||
EVSIKCTLRDLVSKRVTSPE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:|| ||::|| |||||||
EVSIKCTLRDLVSKRVTSPE 301
                                                                                                                                                                                                                                                                                                          1 EVAIKTILKELVHKRVTSPE 20
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                                                                                                                                                                   Query Match 75.3%;
Best Local Similarity 75.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.3
Best Local Similarity 75.0
Matches 15, Conservative
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A29962
A;Molecule type: DNA
A;Residues: 1-668 <REE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S:
Matches 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: minute virus of mice (strain MVMi)
C.Species: minute virus of mice, murine parvovirus
C.Species: minute virus of mice, murine parvovirus
C.Species: minute virus of mice, murine parvovirus
C.Species: 28-06-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
C.Accession: A23008; A2510
R.Sahli, R.; McMaster, G.K.; Hirt, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A.Title: DNA sequence comparison between two tissue-specific variants of the autonomous
A.Reference number: A23008; MUID:85242059; PMID:3855242
A.Accession: A23008, MUID:85242059; PMID:385242
A.Accession: A23008
A.Molecule type: DNA
A.Reference number: A23010; MUID:86115415; PMID:3502703
A.Accession: A29510
A.Accession: A29510
A.Molecule type: DNA
A.Reference number: A23510; MUID:86115415; PMID:3502703
A.Accession: A29510
A.Molecule type: DNA
A.Resession: A29510
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('Species: feline panleukopenia virus, FPLV
('Species: deline panleukopenia virus, FPLV
('Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
('Accession: A03697
Ricarlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J. Virol. 55, 574-587, 1985
A.Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv
A;Reference number: A03697; MUID:85265017; PMID:2991581
                                                                                   noncapsid protein NSI - minute virus of mice
C;Species: minute virus of mice, murine parvovirus
C;Daccies: minute virus of mice, murine parvovirus
C;Accession: A03696
R;Ascession: A03696
R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C.
Nucleic Acids Res. 11, 999-1018, 1983
A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A;Accession: A03696; MUID:83143341; PMID:6298737
A;Molecule type: DNA
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96.9%; Score 94; DB 1;
Best Local Similarity 95.0%; Pred. No. 4e-07;
Matches 19; Conservative 1; Mismatches
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A;Cross-references: EMBL:V01115
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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A; Accession: A03697

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A;Reference number: A48472; MUID:94025614; PMID:8212598
A;Accession: A48472
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50.0%;
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Best Local Similarity 60.0%;
Matches 12; Conservative
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Matches 10; Conserv
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A;Molecule type: DNA
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RiMartyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Virol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvo
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvo
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvo
A;Title: Nucleotide in Mulp: 91073139; PMID:2174965
A;Accession: A36608
A;Molecule type: DNA
A;Residues: 1-668 «MAR»
A;Residues: 1-668 «MAR»
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
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A;Residues: 1-85, R', 87-273,'R',275-375,'V',377-620,'NLH',623-624,'PTPPD',630,'AIR',634,
A;Cross-references: ENBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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N,Alternate names: nonstructural protein NS-1
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Accession: A36217; A48472; A33743
R;Vasudevacharya, J; Basak, S; Srinivas, R.V.; Compans, R.W.
A;Vasudevacharya, J; Basak, S; Srinivas, R.V.; Compans, R.W.
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
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A, Experimental source: strain NADL-2
A, Experimental source: strain NADL-2
Y, Experimental source: strain NADL-2
A, Experimental source: strain NADL-2
A, Titology 197, 86-98, 1993
A, Titology 197, 86-98, 1993
A, Titology 197, 86-98, 1993
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C;Species: porcine parvovins
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 16-Jun-2000
C;Accession: A33302; B36217; A33743; A36217
J; Gen. Virol. 70, 2541-2553, 1989
A;Tille: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
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Pred. No. 0.00095;
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Pred. No. 0.26;
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Best Local Similarity 75.0%;
Matches 15; Conservative
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nes 12; Conservative
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A;Residues: 1-662 <VAS>
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A;Residues: 1-660 <RAN>
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conserved hypothetical protein VC1647 [imported] - Vibrio cholerae (strain N16961 serogrc C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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A,Experimental source: serogroup O1; strain N16961; biotype Bl Tor
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2203
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A;Cross-references: GB:BA000019; PIDN:BAB74879.1; PID:g17132275; GSPDB:GN00179
A;Experimental source: strain PCC 7120
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Roperidues: 1-662 - SER>
A;Experimental source: strain NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
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22;
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                                                                                                                                                                                                                                                                                                     1; Length 662;
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                 Score 58; DB 1
Pred. No. 0.26;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.4%; Score 46; DB 62.5%; Pred. No. 22; ive 1; Mismatches
                                                                                                                                                                                        C; Superfamily: parvovirus noncapsid protein C; Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 EVSIKCTIRDLVNKRCTSIE 299
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R.Hermans, J.; Westhoff, P.
Mol. Gen. Genet. 234, 275-284, 1992
A.Title: Homologous genes for the C(4) isoform of phosphoenolpyruvate carboxylase in a C.
A.Reference number: S25081; MUID:92374996; PMID:1508152
                                                                                                                                                           phosphoenolpyruvate carboxylase (EC 4.1.1.31) isoform C4 (clone ppcA1) - Flaveria trinery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AjIntrone: 56/3; 187/2; 215/3; 291/2; 325/3; 355/1; 406/3; 739/3; 868/3
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
                                                                                                                                                                                       C,Species: Flaveria trinervia
C,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-967 <HER>
A;Cross-references: EMBL:X64143; NID:g18463; PIDN:CAA45504.1; PID:g18464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2; Length 967;
Pred. No. 35;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 28, 2004, 13:00:57 Job time : 12.5 secs
         135 ESDIEETFKRLVHKLNKSPE 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
                                                                                                                                                                                                                                                   C; Accession: S25082
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                                                                                                                               S25082
      셤
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S18318
Subsolve and provide and provided (EC 4.1.1.31) isoform C4 (clone ppc1-1) - Flaveria trine
C;Species: Flaveria trinervia
C;Date: 22-Nov-1993 #sequence revision 23-Feb-1996 #text_change 22-Jun-1999
C;Accession: S18118; S60517; S17342
R;Poetsex, W.; Hermans, J.; Westhoff, P.
FEBS Lett. 292, 133-136, 1991
A;Title: Multiple cDNAs of phosphoenolpyruvate carboxylase in the C(4) dicot Flaveria transference number: S18318; MUID:92070471; PMID:1720398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A;Residues: 1-966 <BAUD.
A;Cross-references: EMBL:Z25853; NID:g397914; PIDN:CAA81072.1; PID:g397915
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
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submitted to the EMBL Data Library, August 1991
A;Description: Multiple cDNAs of the phosphoenolpyruvate carboxylase in the C4 dicot Fla
A;Reference number: S17342
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A;Note: this sequence has been revised in reference 860517
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
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                                                                                                                                                                                                                                                            phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Flaveria australasica C;Species: Flaveria australasica C;Species: Flaveria australasica C;Species: Plaveria australasica C;Accession: S37072
R;Bauwe, H. submitted to the EMBL Data Library, September 1993
A;Reference number: S37072
A;Reference number: S37072
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Cross-references: EMBL:X61304; NID:g498699; PIDN:CAA43601.1; PID:g498699
Note: this is a revision to the sequence from reference S17342
      Gaps
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A,Note: only a part of the coding sequence is given in this paper R,Poetsch, W.
Submitted to the EMBL Data Library, June 1994
A,Reference number: 860517
A,Accession: S60517
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Pred. No. 35;
1; Mismatches 8; Indels
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47.4%; Score 46; DB 2; Length 966;
Best Local Similarity 55.0%; Pred. No. 35;
Matches 11; Conservative 1; Mismatches 8; Indels
      5; Indels
Mismatches
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157 EIALSSPSYELIHKRRTS 174
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Best Local Similarity
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A;Residues: 1-966 <POE>
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Gaps

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GenCore version 5.1.6
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US-10-069-056-5 97 1 EVAIKTTLKELVHKRVTSPE 20 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ð			SUMMARIES	
Result		Query				
NO.	Score	Match	Match Length	DB	αī	Description
-	94	96.9	899	-	VNCS PAVL3	311 par
7	94	96.9	672	Н	VNCS MUMIM	_
e	94	9	672	-	VNCS_MUMIV	P03134 murine minu
4	94	9	672	Н	VNCS_PAVHH	3 hamster
2	73	75.3	392	Н	VNCS_FPV	Н
9	73	S	668	н	VNCS_FPV19	2 feline
7	73	75.3	668	Н	VNCS MEVA	
80	73	5	668	Н	VNCS PAVCN	
6	58	59.8	099	-	VNCS_PAVPN	
10	58	59.8	662	н	VNCS PAVPK	porcine
11	46	47.4	192	Н	Y525_BUCAP	buchnera
12	46	47.4	996	Н	CAP2_FLATR	flaveria
13	46	47.4	996	Н	CAPP_FLAAU	
14	46	47.4	. 196	н		
15	45	46.4	777	Н	HEXA_PORGI	
16	45	46.4	2541	Н		
17	45	46.4	2541	Н		
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26	41	•	200	Н	VIP_MELGA	meleag
27	41	•	264	-	SURE HELHP	helicoba
28	41		1361	-1	GLI4_XENLA	Q91661 xenopus lae
29	40	41.2	207	Н	UPP MYCTU	-
30	40	41.2	238	٦	YC53_PORPU	P51202 porphyra pu
31	40	•	385	~		
32	40	41.2	488	Н		0
33	40	41.2	561	Н	Y423_MYCPN	P75174 mycoplasma

O26541 methanobact Q96yq8 arabidopsis	P23579 euglena gra Q97eg9 clostridium P47310 mycoplasma	Q96dt5 homo sapien Q9zmu4 helicobacte	PS5979 helicobacte Q20140 caenorhabdi	094404 schizosacch Q9bxy5 homo sapien
UVRC_METTH CLV1_ARATH	RPOB_EUGGR RPOB_CLOAB Y064_MYCGE	DYHB_HUMAN BCP_HELPJ	BCP_HELPY KADI_CAEEL NY DO MOTICE	YJ3C_SCHPO CAY2_HUMAN
579 1 980 1	1082 1 1241 1 1331 1	4523 1 152 1	210 1	278 1 382 1
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ALIGNMENTS

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		. (6	protein NS1).		/irinae; Parvovirus				Ĩ.;	of parvovirus LuIII and	e for			-1- FUNCTION: Seems necessary for viral DNA replication.	 -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family. 		This SWISS-PROT entry is copyright. It is produced through a collaboration	between the Swiss Institute of Bioinformatics and the EMBL outstation	the European Bioinformatics Institute. There are no restrictions on	by non-profit institutions as long as its content is in no	modified and this statement is not removed. Usage by and for commercial	10.D://www.18D-81						Nonstructural protein; Noncapsid protein; DNA replication;		•	CAE69049F8F86B53 CRC64;	l; Length 668;	0; Indels	
668 AA.	indate)				; Parvov				ederma N	parvovi	saibly r			ral DNA	viruses		It is pr	nformati	e. Ther		emoved.	ין ואפני ז סאין	CII.) .					tein; DN		ATP (POTENTIAL)	049F8F86	Score 94; DB 1;	Fred. No. 2e-U7; ; Mismatches	
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STANDARD;	29, Created)	Last	NOI		ssDNA viruses; Parvoviridae; Parvovirinae;			יייש-משליי	C., Bates	otide sec	nique sec	rn.";	5(1993).	песевват	ongs to t		ry is cor	Institute	ormatics	institu	tatement	license	Trense	T ANNOTAL	١.	; Parvo N	o_NS1; 1.	in; Nonce		406	75846 MW;	96.98;	95.0%; ative	
STAN	(Rel.	(Re1.	rotein N	Lulii.	DNA viru	35339;	:	OM N.A.	Chen K.	te nucle	nofau	on patte	2:339-34	N: Seems	ITY: Bel	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PROT ent	e Swiss	n Bioint	n-protit	d this s	quires a	email co	8; -; NO	; A44276	PR001257	57; Parv	al prote			668 AA;	:	Similarity 95.	
T 1 PAVL3 VNCS PAVL3	01-JUN-1994	15-DEC-1998	Noncapsid protein	Parvovirus LuIII	Viruses; ss	NCBI_TaxID=35339;	[1]	SEQUENCE FROM N.A. MEDIINE-93297126: Dubmed-9617035:	Diffoot N., Chen K.C., Bates R.C., Lederma M.;	"The complete nucleotide sequence	localization of a unique	encapsidation pattern.";	Virology 192:339-345(1993).	-!- FUNCTIO	-!- SIMILAR		This SWISS-	between th	the Europea	use by no	modified and this statement is not removed.	entities reduites a incense agreement to	or sellu all email to ilcense@isb-sib.cm/.	EMBL; M81888; -; NOT ANNOTATED CDS.	PIR; A44276; A44276.	InterPro; IPR001257; Parvo NS1	Pfam; PF01057; Parvo_NS1;	Nonstructur	ATP-binding		SEQUENCE		Best Local Sim: Matches 19;	
RESULT 1 VNCS PAV ID VNC	25	占	B 8	s S	႘	ŏ	Z :	RP v	æ	RT	RT	RT	RL	ပ္ပ	ខ្ល	ဗ	ខ	ខ្ល	ខ្ល	ខ្ល	ខ្ល	3 5	3 5	S &	DR	DR	DR	¥	Š	FT	Ö	Que	Bee	

1 EVAIKTTLKELVHKRVTSPE 20 ||:||||||||||||| 281 EVSIKTTLKELVHKRVTSPE 300 Š a

"VNCS MUMIM STANDARD; PRT; 672 AA. P0730; P10837; 01-APR-1988 (Rel. 07, Created) 01-UUL-1989 (Rel. 11, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) RESULT 2
VNCS_MUMIM
ID VNCS MU
AC P07300,
DT 01-JUEDT 15-DEC-

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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                            autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:3617-3633(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                     MEDLINE-85242059; PubMed=3855242;
Sahli R., McMaster G.K., Hirt B.;
"DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                Astell C.R., Gardiner B.M., Tattersall P., "DNA sequence of the lymphotropic variant of minute virus of min
WM(i), and comparison with the DNA sequence of the fibrotropic
                       Murine minute virus (strain MVMi) (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.9%; Score 94; DB 1; Length 672; 95.0%; Pred. No. 2e-07;
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76140 MW; 25F025FE328B4DF0 CRC64;
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Nucleic Acids Res. 11:999-1018(1983)
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                                                                                       MEDLINE=86115415; PubMed=3502703;
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                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                         prototype strain.";
J. Virol. 57:656-669(1986).
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les 19; Conserv
                                                                        SEQUENCE FROM N.A.
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P03134;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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-!- FUNCTION: Seems necessary for viral DNA replication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10799;
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0
                                                                                                                                                                                    EMBL; J02275; AAA67109.1; -.
EMBL; V01115; CAA24309.1; ALT_INIT.
PIR; A03696; UTVPIM.
TRANSFAC; T02375; -.
InterPro; IPRO1057; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; T.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-19966 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X01457; CAA25689.1; -.
PIR; A03695; UYPVV1.
InterPro; IPR001257; Parvo NS1.
Pfam; PP01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.9%; Score 94; DB 1; Length 672; 95.0%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       76248 MW; 50298F27662E3C1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75993 MW; 12F331142F72AA6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.9%; Score 94; DB 1; 95.0%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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MEDLINE=83112183; PubMed=6823009;
Rhode S.L. III, Paradiso P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 EVSIKTTLKELVHKRVTSPE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVAIKTTLKELVHKRVTSPE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          672 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=91202123; PubMed=2016597;
Kariatsumari T., Horiuchi M., Hama B., Yaguchi K., Ishigurio N.,
Goto H., Shinagawa M.;
"Construction and nucleotide sequence analysis of an infectious DNA
clone of the autonomous parvovirus, mink enteritis virus.";
J. Gen. Virol. 72:867-875(1991).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                      "Mapping specific functions in the capsid structure of canine parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
NCBI_TaxID=10793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
1-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 1; Length 668;
Pred. No. 0.00051;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76768 MW; 4F8FEA3EE62D2AE7 CRC64;
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N -> D (IN REF. 2).

I -> V (IN REF. 2).

I -> N (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X55115; CAA38910.1; -.
EMBL; M38246; AAC37927.1; -.
PIR; A36608; UVPVFP.
InterPro; IPR00359; AAA_ATPage.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
J. Gen. Virol. 71:2747-2753(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 EVSIKCTLRDLVSKRVTSPE 301
                                                                              MEDLINE=91272479; PubMed=1647068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVAIKTILKELVHKRVISPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.3%;
                                                                                                                                                                                Virology 183:195-205(1991).
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Best Local Similarity 75.0
Matches 15; Conservative
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443
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 4
575 5
668 AA;
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                                         SEQUENCE FROM N.A.
                                                                                                     Parrish C.R.;
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                                                                                                                                                               clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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                                                                                                                                                                                                                                                                                                                                                              Hahn W.;
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-8525017; PubMed=2991581;
Carlson J., Rubshlow K., Maxwell I., Maxwell F., Winston S., Hahn
"Cloning and sequence of DNA encoding structural proteins of the
autonomous parvovirus feline panleukopenia virus.";
                                                                                                                                                                                                                             Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBL_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   openia Virus (strain 193) (FFV).
Viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                    01-JAN-1988 (Rel. 06, Created)
1-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.3%; Score 73; DB 1; Length 392; 75.0%; Pred. No. 0.0003; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
1-MAR-1992 (Rel. 21, Last sequence update)
15-DBC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                        J. Virol. 55:574-587(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 AA; 43971 MW; B875ADDB4977F616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feline panleukopenia virus (strain 193) (FPV)
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                                                                                392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
SWART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVAIKTILKELVHKRVTSPE 20
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                                                                                STANDARD;
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P24842;
                                                                                                                                                                                                      (Fragment).
                                       RESULT 5
VNCS_FPV
ID _VNCS_FPV
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SEQUENCE Query Match

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VNCS FPV19
ID VNCS FP
DT O1-MAR.
DT 01-MAR.

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Gaps

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282 EVSIKCTLRDLVSKRVTSPE 301

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    (See http://www.isb-sib.ch/announce/
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MEDLINE-88062922; PubMed-2824850;
Reed A.P., Jones E.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
                                                                                                                                                                                                     Nonstructural protein; Noncapsid protein; DNA replication; ATP-binding.
                                                                                                                                                                                                                                                                                                                       75.3%; Score 73; DB 1; Length 668; 75.0%; Pred. No. 0.00051; Live 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                    400 407 ATP (POTENTIAL).
668 AA; 76736 MW; DBD5F9E92113685C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 407 ATP (POTENTIAL).
668 AA; 76764 MW; DE2CCEA69D2A63A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 AA.
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                             EMBL; D00765; BAA00662.1; -.
PIR; A38350; UYPVME.
InterPro; IPR001359; AAA ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; I.
SMART; SM00392; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine parvovirus (strain N) (CPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                         282 EVSIKCTLRDLVSKRVTSPE 301
                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVAIKTTLKELVHKRVTSPE 20
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InterPro; IPR00359; AAA_ATPase.
InterPro; IPR001557; Parvo_NS1.
Pfam; PP01057; Parvo_NS1.
SMART; SM00382; AAA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M19296; AAA67459.1; -. EMBL; M38245; AAB02798.1; -.
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 15; Conserv
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P12929;
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@18b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 367-660 FROM N.A.
MEDLINE=90085785; PubMed=2596019;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
"Nucleotide sequence analysis of the capsid genes and the right-hand terminal palindrome of porcine parvovirus, strain NADL-2.";
Virology 173:368-377(1989).
-1- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=91021005; PubMed=2219713; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Tasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Tasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Tasudevacharya Sequence of an infectious clone of porcine parvovirus, strain NADL-2."; Virology 178:611-616(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALY (POIGNITAL).

G -> R (IN REF. 2).

K -> V (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNTDT -> NLHLTPTPPDSAIRTP (IN
                                                                                                                                                                                                             Porcine parvovirus (strain NADL-2) (PpV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10797;
                                                                                                                                                                                                                                                                                                                                                                                                    Ranz A.I., Manclus J.J., Diaz-Aroca E., Casal J.I.;
"Porcine parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M32787; AAA46916.1; -.
PIR; A33302; UYPVPP.
Therbro; DR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.8%; Score 58; DB 1; Length 660; 60.0%; Pred. No. 0.13; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF. 2).
75300 MW; C0B1DF2226A2EF0A CRC64;
VNCS_PAVPN STANDARD; PRT; 660 AA.
P18547; P22965;
01-NOV-1990 (Rel. 16, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1)
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90010964; Pubmed=2794971;
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ses 12; Conserv
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Gaps

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2; Indels

3; Mismatches

1 EVAIKTTLKELVHKRVTSPE 20

Local Similarity 75.0 nes 15; Conservative

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Pfam; PF00311; PEPcase; 1.
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                                                                                                                                                                                                                                                                                   RESULT 12
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                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22084549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
Science 296:2376-2379(2002).
-! SIMILARITY: STRONG, TO E.COLI YHGI AND H.INFLUENZAE H10433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                        MEDLINE=96183900; PubMed=8642680;
Bergeron J., Hebert B., Tijssen P.;
"Genome organization of the Kresse strain of porcine parvovirus:
identification of the allotropic determinant and comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                           Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 1; Length 662; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural protein; Noncapsid protein; DNA replication; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                        those of NADL-2 and field isolates.";
J. Virol. 70:2508-2515(1996).
-!- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        B53F76D9F9FBD613 CRC64;
                                01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.13;
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18-FEB-2003 (Rel. 41, Last annotation update)
BUSG525.
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            662 AA.
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                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                               Porcine parvovirus (strain Kresse) (PPV)
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Pfam; PF01057; Parvo NS1; 1.
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Best Local Similarity 60.vv,
Best Local 12; Conservative
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            STANDARD;
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                                                                                                                       NCBI_TaxID=73487;
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(See http://www.isb-sib.ch/announce/
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it forms oxaloacetate, a four-carbon dicarboxylic acid source for
the tricarboxylic acid cycle.
-i- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
phosphoenolpyruvate + CO(2).
-i- ENZYME REGULATION: By light-reversible phosphorylation.
-i- PATHWAY: Tricarboxylic acid cycle.
-i- SUBUNIT: Homotetramer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJNE=92070471; PubMed=1720398;
Poetsch W., Hermans J., Westhoff P.;
"Multiple cDNAs of phosphoenolpyruvate carboxylase in the C4 dicot
institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 192;
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28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poetsch W.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                  ProDom; PD002830; NifU C; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 192 AA; 21665 MW; 7C3E41BC59D2FBDC CRC64;
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-!- SIMILARITY: Belongs to the PEPCase family.
                          modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              47.4%; Score 46; DB : 57.9%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                      InterPro; IPR000361; HesB yadR_yfhP InterPro; IPR001075; NifU_C.
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                                                                                                                                                         EMBL; AE014127; AAM68067.1; -.
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                                                                                                                                                                                                                                                    Pfam; PF01521; HesB-like; Pfam; PF01106; NifU-like;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.9.
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non-profit
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1; Length 966;

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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PRINTS, PR00150; PEPCARBXLASE.
PROSITE; PS00393; PEPCASE_2; 1.
PROSITE; PS00781; PEPCASE_1; 1.
Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Tricarboxylic acid cycle. This isozyme is involved in C4
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Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.

MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).

ACT_SITE 172 BY SIMILARITY.

ACT_SITE 600 600 BY SIMILARITY.

SEQUENCE 966 AA; 110405 MW; 252DB9E9070BC109 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterid campanulids, Asterales, Asteraceae, Asteroideae, Tageteae, Flaveria.
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ENZYWE REGULATION: By light-reversible phosphorylation (By
                                                                                                                           Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                      47.4%; Score 46; DB 1; Length 966; 55.0%; Pred. No. 17; sive 1; Mismatches 8; Indels
                                                                                                                                                                                                172 172 BY SIMILARITY.
600 600 BY SIMILARITY.
966 AA; 110406 MW; 252F7B674BC94F47 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the PEPCase family.
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PROSITE; PS00393; PEPCASE 2; 1.
PROSITE; PS00781; PEPCASE 1; 1.
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Pfam; PF00311; PEPcase; 1.
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Best Local Similarity 55.0°,
Tropes 11; Conservative
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Q42730;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92374996; PubMed=1508152;
Hermans J., Westhoff P.;
"Homologous genes for the C4 isoform of phosphoenolpyruvate
carboxylase in a C3 and a C4 Flaveria species.";
Mol. Gen. Genet. 234:275-284(1992).
-!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
it forms oxaloacetate, a four-carbon dicarboxylic acid source for
the tricarboxylic acid cycle.
-!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
phosphoenolpyruvate + CO(2).
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENZYME REGULATION: By light-reversible phosphorylation.
PATHWAY: Tricarboxylic acid cycle. This isozyme is involved in C4
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PROSITE; PS00391; PEPCASE 2; 1.
Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
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Pred. No. 17;
1; Mismatches 8; Indels
                                                                    Indels
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase).
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BY SIMILARITY.
1; 61E8A493842E1C1F CRC64;
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--- SUBUNIT: Homotetramer.
--- SUBCINIT: Homotetramer.
--- SUBCILULAR LOCATION: Cytoplasmic.
--- TISSUB SPECIFICITY: Mesophyll cells of leaves.
--- SIMILARITY: Belongs to the PEPCase family.
Score 46; DB 1
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                             967 AA.
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ESDIEETFKRLVHKLNKSPE 154
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135 ESDIEETFKRLVHKLNKSPE 154
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InterPro; IRRO1449; PEPcase.
Pam; PF00311; PEPcase; 1.
PRINTS; PR00150; PEPCARBXLASE.
                                55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M., Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J., Dewhirst P.B., Tetelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M.;

"Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";

J. Bacteriol. 165:5591-5601(2003)

-!- CATALYTITY: Hydrolysis of terminal non-reducing N-accetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
                                                                                                                                                                                                                                                                                 Lovatt A., Roberts I.S.; "Cloning and expression in Escherichia coli of the nahA gene from Porphyromonas gingivalis indicates that beta-N-acetylhexosaminidase is an outer-membrane-associated lipoprotein."; Microbiology 140:3399-3406(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA-HEXOSAMINIDASE.
N-palmitoyl cysteine (Probable).
S-diacylglycerol cysteine (Probable).
                           01-FEB-1996 (Rel. 33, Created)
10-GCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
Beta-hexosaminidase precursor (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase) (Beta-GlcNAcase) (Beta-N-acetylhexosaminidase)
                                                                                                                                              Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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Hydrolase; Glycosidase; Signal; Outer membrane; Lipoprotein;
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T -> S (IN REF. 1).
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777 AA
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InterPro; IPR00437; Prok lipoprot_S.
Pfam, PF00728; Glyco_hydro_20; 1.
Pfam; PF02838; Glyco_hydro_20b; 1.
PRINTS; PR00738; GLHYDRLASE20.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=W83;
MEDLINE=22829867; PubMed=12949112;
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 HEXA PORGI
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  DB 1; Length 777;
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Query Match
Best Local Similarity 40.9%; Pred. No. 20;
Matches 9; Conservative 8; Mismatches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

Gaps STRAIN=Yale;
MEDLINE=Z1102993; PubMed=11172095;
MEDLINE=Z1102993; PubMed=11172095;
MEDLINE=Z1102993; PubMed=11172095;
MEDLINE=Z1102993; PubMed=11172095;

Ball-Goodrich L.J., Johnson E., Jacoby R.;
Darvoviruses of rats.",
J. Gen. VIrol. 82:537-5401.
InterPro; IPR001257; Parvo_NS1.
InterPro; IPR01257; Parvo_NS1.
SEQÜENCE 397 AA, 43959 MW; D62052E4767366BB CRC64; Autonomous rat parvovirus RV-Y. Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. NCBI_TaxID=155025; ö Query Match 96.9%; Score 94; DB 12; Length 397; Best Local Similarity 95.0%; Pred. No. 4.9e-07; Matches 19; Conservative 1; Mismatches 0; Indels 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Nonstructural protein 1 (Fragment). 397 AA. PRT; 1 EVAIKTTLKELVHKRVTSPE 20 EVSIKTTLKELVHKRVTSPE 25 PRELIMINARY; SEQUENCE FROM N.A. Q993M6 RESULT 1

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665 AA.

PRT;

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Gaps

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Length 672;

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SEQUENCE FROM N.A.
MEDLINE=9436551; PubMed=8083985;
Ball-Goodrich L.J., Johnson E.;
"Molecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).
                          Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=35340;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
                                                                                                                                  Brown Like A.A.;
Brown Cof a Diabetogenic Parvovirus of Rats.";
"Sequence of a Diabetogenic Parvovirus of Rats.";
Submitted (NOV.1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U79033; AAB38326.1; -.
Interbro; IRR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
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Ball-Goodrich L.J.;
Ball-Goodrich L.J.;
Submitted (JUL.1914) to the EMBL/GenBank/DDBJ databases.
EMBL; U12463, AAA614405.1; -.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; J.
SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Nonstructural protein 1.
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95.0%; Pred. No. 8.1e-07;
tive 1; Mismatches 0;
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Best Local Similarity 95.0%;
Matches 19; Conservative
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                    Kilham rat virus.
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                                                                                                                  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=172385;
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Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
EMBL; AA932882; AAM93275.1; -.
InterPro; IPR01127; Parvo NS1.
Pfam; PF01077; Parvo NS1; I.
SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      665 AA; 75375 MW; 778E29043417E409 CRC64;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nonstructural protein (Fragment).
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
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J. Virol. 72:3289-3299(1998).
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Kilham rat virus,
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InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; \( \frac{1}{1}\).
SEQUENCE 672 AA; \( \frac{7}{6}\)201 MW; C2F1A71F6EF449A6 CRC64;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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NCBI_TaxID=172386;
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                                         Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K., "Molecular characterization of three newly recognized rat
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                                                                                                                                                                                                                           0; Indels
                                                                                parvoviruses.";
J. Gen. Virol. 83.2075-2083(2002).
BMBL; A7321230, AAM93272.1; -.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 75987 MW; 2284611C20CDB6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).

EMBL, AA932884; AAM93279.1; -.
InterPro; IPR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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J. Gen. Virol. 83:2075-2083(2002).
EMBL; AF332883; AAM93277.1; -.
                       MEDLINE=22120170; PubMed=12124471;
                                                                                                                                                                                                                                                                                                                                            281 EVSIKTTLKELVHKRVTSPE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 95.09
....hes 19; Conservative
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nes 19; Conservative
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Rat minute virus 1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=172387;
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of mice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MVM(p);
MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MVM(p);
MEDLINE=86115415; PubMed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mic
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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Match 96.9%; Score 94; DB 12; Length 672; Local Similarity 95.0%; Pred. No. 8.1e-07; les 19; Conservative 1; Mismatches 0; Indels
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Pfam; PF01057; Parvo NSI; 1.
SEQUENCE 721 AA; 81896 MW; 18391758E42F0DCF CRC64;
                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nonstructural protein.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parvovirus.";
Nucleic Acids Res. 11:999-1018(1983)
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                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                     281 EVSIKTTLKELVHKRVTSPE 300
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                                                                                                          1 EVAIKTTLKELVHKRVTSPE 20
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les 19; Conservative
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"Evolutionary pattern of feline panleukopenia virus differs from that
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VGSI_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                niteuropenia viius (FFV);
ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.3%; Score 73; DB 12; Length 668; 75.0%; Pred. No. 0.0023; Live 3; Mismatches 2; Indels
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                                                                                                                                                                           of canine parvovirus.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000015; BAA19018.1;
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR001593; AAA_ATPase.
InterPro; IPR00157; Parvo NS1.
Fiam; PF01057; Parvo NS1.
Fiam; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000069; BAA19030.1; -.
EMBL; AB000063; BAA19024.1; -.
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668 Aa; 76769 MW; OECAFEGBF62ASDE0 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Nonstructural protein 1.
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GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR001359; AAA ATPase.
InterPro; IPR001257; Parvo NSI.
Pfam; PP01057; Parvo NSI.
SMART; SM00382; AAA; I.
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les 15, Conservative
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nes 15; Conservative
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              [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                              STRAIN=PLI-IV;
Horiuchi M.;
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Matches
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P90472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                             STRAIN=1ymphotropic variant,
MEDLINE=66115415; Pubmed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.,
"DNA sequence of the lymphotropic variant of minute virus of mice,
"MW(!), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horiuchi M.;

"Evolutinary pattern of feline panleukopeina virus differs that of canine parvovirus.";

"Evolutinary pattern of feline panleukopeina virus differs that of submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; AB000062; BAA19023.1;

Therpro; IPR001257; Farvo biding; IEA.

InterPro; IPR001257; Parvo NS1.

Fran; PF01057; Parvo NS1.

Shart; SM00382; AAA; 1.

SEQUENCE 668 AA; 76755 MW; 37ABDFD347017F52 CRC64;
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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NCBI_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 96.9%; Score 94; DB 12; Length 721; Local Similarity 95.0%; Pred. No. 8.7e-07; hes 19; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 721 AA; 81863 MW; 9FD29C327C7F4BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 EVSIKCTLRDLVSKRVTSPE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVAIKTTLKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feline panleukopenia virus (FPV)
                                                                                                                                                                                                                                                                                                                                               prototype strain.";
J. Virol. 570:656-669(1986).
EMBL: M12032; AAAG9566.1; -.
EIR; A23008; UYPVIM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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P89516
AC P89511
AC P8951
DT 01-MA
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RESULT 12 P89515

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                                                                                                                                                                                                          Gaps
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0
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
                    E SUBMITCHE (17AN-1997) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB000065; BAA19028-1; -

R EMBL; AB000065; BAA19028-1; -

R GO; GO:0001065; BAA19026-1; -

R GO; GO:0001065; F:nucleotide binding; IEA.

R InterPro; IPR001557; AAA_ATPasse.

R InterPro; IPR001557; Parvo NS1.

R SMART; SMO0382; AAA, 1.

NOMETRICURAL PROTECHI.

NOMETRICURAL PROTECHI.

SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
                                                                                                                                                                              Query Match 75.3%; Score 73; DB 12; Length 668; Best Local Similarity 75.0%; Pred. No. 0.0023; Matches 15; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.3%; Score 73; DB 12; Length 668; Best Local Similarity 75.0%; Pred. No. 0.0023; Matches 15; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-1997 (TrEWBLrel. 03, Created)
01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                282 EVSIKCTLRDLVSKRVTSPE 301
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                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Fukagawa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horiuchi M.;
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P89513;
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Search completed: May 28, 2004, 13:00:02 Job time : 33 secs

282 EVSIKCTLRDLVSKRVTSPE 301

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Sequence 745,

Sequence Sequence 6, Appli 6, Appli 23671, A 5997, Ap 66, Appli 2, Appli

Sequence (Sequence Sequence

Appl Appl Appl Appl Appl Appl

Sequence 1003 Sequence 11, Sequence 16, Sequence 98, Sequence 15, Sequence 15,

Run

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JOHERANT INFORMATION STRUCT

APPLICANT: Caplinski, Kevin

APPLICANT: Caplinski, Kevin

APPLICANT: Caplinski, Kevin

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 60.1.1-85N

CURRENT APPLICATION NUMBER: US/09/359,268A

CURRENT APPLICATION NUMBER: US/09/359,268A

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 26

LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 60134520 No. 6013452disk of No. 6013452th America, Inc. STREET: 405 Lexington Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
44.8%; Score 43.5; DB 4; Length 472;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 14; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09079415
Patent No. 6013452
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christensen, Tove
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: A Fungus Wherein The area, pepC and/or
TITLE OF INVENTION: pepE Genes Have Been Inactivated
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  US-08-818-823-6
US-09-252-991A-23671
US-09-543-681A-5997
US-09-914-259-66
US-09-614-480-2
                                      US-09-543-681A-7151
US-09-134-001C-5071
US-09-198-452A-1003
US-09-080-983-11
US-09-880-463A-14
US-09-360-197-16
US-07-861-458C-98
US-09-651-656-15
US-09-651-656-15
US-08-480-101-14
US-08-480-101-14
-09-198-452A-745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-359-268A-26
; Sequence 26, Application US/09359268A
; Patent No. 6630294
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: saccharomyces cerevisiae
\begin{smallmatrix} \mathbf{q} & \mathbf{q} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New YOUTHE: NY COUNTRY: US. ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-359-268A-26
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US-09-079-415-2
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Sequence 6583, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 247, App
Sequence 247, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 100, App
Sequence 100, App
Sequence 11, Appli
Sequence 6712, Ap
Sequence 611, Appli
Sequence 3, Appli
Sequence 3, Appli
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11778, A
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5150, Ap
5739, Ap
4162, Ap
5738, Ap
5746, Ap
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                                                                                                                                                  May 28, 2004, 12:53:44 ; Search time 13.5 Seconds (without alignments) 76.483 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-079-415-2
US-09-079-415-2
US-08-392-362-4
US-08-392-362-4
US-08-473-553A-4
US-08-473-553A-6
US-08-473-553A-6
US-08-473-553A-6
US-08-473-553A-6
US-08-473-553A-6
US-08-800-506-11
US-08-680-506-11
US-08-680-506-3
US-08-680-506-3
US-08-680-506-3
US-08-99-138-6
US-09-489-039A-11778
US-09-489-039A-11778
US-09-138-6
US-09-353A-5724
US-09-107-533A-5724
US-09-114-00C-5150
US-09-621-976-4162
US-09-621-976-4162
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US-09-107-532A-5053
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                  389414 segs, 51625971 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                    1 EVAIKTTLKELVHKRVTSPE
                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                  US-10-069-056-5
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Match Length
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                                                                                                                                                                                                                                                                                                                                  Scoring table:
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Maximum DB
                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
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46.7%; Pred. No. 1.6e+02;
tive 5; Mismatches 3; Indels
                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-00-392-362-4
; Sequence 4, Application US/09392362
; Patent No. 6248868
; GENERAL INFORMATION:
    TITLE OF INVENTION: PHRAGMOPLASTIN
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: CALFEE, HALTER & GRISWOLD
; STREET: 800 SUPERIOR AVENUE

CITY: CLEVELAND
                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLLICK, MARY E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: GOLRICK, MARY E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/799,138
                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: : ||:||| ::
428 AVHSLLKDLVHKAIS 442
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                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 610 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                             COMPUTER READABLE FORM:
             CLEVELAND
                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                         44114
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44114
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                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-799-138-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.3%; Score 41; DB 4; Length 198; 56.2%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                       OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/079,415 FILING DATE: 14 MAY-1998 CLASSIFICATION: NAME: NOSCK, CATOI REGISTRATION NUMBER: 36,993 REFERENCE/DOCKET NUMBER: 4657.204-US TELEPHONE: 212-867-0123 TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08799138
Patent No. 5994053
GENERAL INFORMATION:
APPLICANT: Verma, Desh Pal
TITLE OF INVENTION: PHRAGMOPLASTIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE: ADDRESSEE: CALFEE, HALTER & GRISWOLD
STREET: 800 SUPERIOR AVENUE
                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-415-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||| ||| ||| |||| 136 VVDKTTNKELAHYKLT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|: ||| ||::| :
292 IALATTLAELINKEI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAIKTTLKELVHKRVT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAIKTTLKELVHKRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-543-681A-6583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-799-138-4
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PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-473-553A-4
                                                                                                                                                                                                                                                                                                                                                                                     unknown
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: un
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TOPOLOGY: un)
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                                                                                                                     Length 610;
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Pred, No. 66;
                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEB: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSEE: Flahr, Hobbach, Test, Albritton & Herber
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/99/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR APPLICATION NUMBER: 60/066,517
NUMBER OF SEQ ID NOS: 437
SOFTWARE: PASTSEQ FOR Windows Version 4.0
                                                                                                                   Score 41; DB 3; I
Pred. No. 1.6e+02;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                           Sequence 247, Application US/09199637A Patent No. 6355411 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08473553A Patent No. 5859338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                     Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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428 AVHSLLKDLVHKAIS 442
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Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                     3 AIKTTLKELVHKRVT 17
LENGTH: 610 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drenkard, Eliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| | |: :|:||
18 IKHLAHRELTTPE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States ZIP: 94111-4187
                                   TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-392-362-4.
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                        US-09-199-637A-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-08-473-553A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 247
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08473553A
Patent No. 585938
GENERAL INFORMATION:
APPLICANT: Myserowitz, Elliot M.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A FILING DATE: 06-JUN-1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
NAME: S11va, RObin M.
REGISTRATION NUMBER: 38,304 REFERENCE/DOCKET NUMBER: A.60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.2%; Score 40; DB 2; Best Local Similarity 35.0%; Pred. No. 1e+02; Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-60886/RFT/RMS
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REFERENCE/DOCKET NUMBER: A-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) /__
TELEPHONE: (415) 398-3249
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APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
NUMBER OF SEQUENCES: 117
                                                                                                                                                                                                                                                                                      Query Match
40.7%; Score 39.5; DB 4; Length 424;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION TOWNER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
; CURRENT APPLICATION NUMBER: US/09/489,039A; CURRENT FILING DATE: 2000-01-27; PRIOR APPLICATION NUMBER: US 60/117,747; PRIOR FILING DATE: 1999-01-29; NUMBER OF SEQ ID NOS: 14342; SEQ ID NO 12030; LENGTH: 424; TYPE: PRT
; CRGANISM: Klebsiella pneumoniae
US-09-489-039A-12030
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Patent No. 5616500
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         146 EVPLLAVISELVH-RYRSPE 164
                                                                                                                                                                                                                                                                                                                                                                                           1 EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIHOS
TELEPONOMINICATION INFORMATION:
TELEPRAS. (714) 760-0404
INFORMATION FOR SEQ ID NO: 100:
SEQUIENCE CHARACTERISTICS:
LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KTTLKELVHKRVTS 18
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Best Local Similarity 57.1
Matches 8; Conservative
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; FRAGMENT TYPE:
US-08-056-200-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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Refert No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001
                                                                                                                                  0
                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                       Query Match
41.2%; Score 40; DB 2; Length 980;
Best Local Similarity 35.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.2%; Score 40; DB 2; Length 985; 35.0%; Pred. No. 3.6e+02; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATHOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-UNN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
ARGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
REPERBENCE/DOKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
TENERY: 985 amino acids
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08473553A Patent No. 5859338 GENERAL INFORMATION:
                                                                                                                                                                                                                 | | : |::|:||
953 EAARPTMREVVHMLTNPPK 972
                                                                                                                                                                               1 EVAIKTILKELVHKRVTSPE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 EAAARPTMREVVHMLTNPPK 977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 985 amino acids
amino acid
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COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.0
Matches 7; Conservative
; MOLECULE TYPE: protein US-08-473-553A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILJ
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
SEQ ID NO 6712
LENGTH: 246
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.6e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 40.2%; Score 39; DB 4; Length 246; Best Local Similarity 41.2%; Pred. No. 1.3e+02; Matches 7; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                    Score 39; DB 3; Length 151;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
CURRENT FILING DATE: 1996-07-08
BARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6712, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVAIKTTLKELVHKRVTSP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QVAFLTCSYELAIKNVTSP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 VEVNĽKLĽVROKITLPE 228
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ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.2%;
58.3%;
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.69
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                     TYPE: PRT
, ORGANISM: Gallus gallus
US-08-680-506-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-543-681A-6712
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                                                                                                                                                                                                                                                              APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-11
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Pred. No. 23;
2; Mismatches
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TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176(5091
CURRENT APPLICATION NUMBER: US/08/680,506C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08680506C Patent No. 6008013 GENERAL INFORMATION:
                                                                                                                                                                          Sequence 100, Application US/08800644
Patent No. 5958752
GENERAL INFORMATION:
     29 KKELKELIQKELTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KTTLKELVHKRVTS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-800-644-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92660
                                                                                                                                                        US-08-800-644-100
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US-08-680-506-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Sequence 801, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:
APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: 031-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849 ö 0; Gaps

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Search completed: May 28, 2004, 13:02:03 Job time : 14.5 secs

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May 28, 2004, 12:57:09; Search time 34.75 Seconds (without alignments) 160.719 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US60_PUBGOMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1151071 seqs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:
                                                                                                                                                                                                                        OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 369, App Sequence 2145, App Sequence 2650, Appl Sequence 2650, Appl Sequence 9876, App Sequence 155727, Sequence 282637, Sequence 282638, Sequence 162905, Sequence 253110, App Sequence 253110, App Sequence 1180, App Sequence 64861, App Sequence 64861, App Sequence 626171, App Sequence 626994, Appli Sequence 65444, App Sequence 65444, App Sequence 65699, Appli Sequence 65699, Appli Sequence 65699, Appli Sequence 65699, Appli	164, 5195 6342 5956
2 US-10-363-616-369 5 US-10-369-493-2145 2 US-10-264-237-2650 4 US-10-264-237-2650 4 US-10-156-761-9876 2 US-10-424-599-185727 2 US-10-424-599-185727 2 US-10-424-599-180339 0 US-10-424-599-180339 0 US-10-424-599-180339 0 US-10-424-599-162035 2 US-10-424-599-162035 2 US-10-424-599-162035 2 US-10-424-599-162035 2 US-10-282-122A-64661 1 US-09-833-245-1380 1 US-10-282-1122A-665307 2 US-10-282-1124-6294 4 US-10-282-1122A-65307 2 US-10-282-112A-65307 2 US-10-282-112A-65307 2 US-10-282-112A-65307 2 US-10-282-112A-65307 2 US-10-282-112A-65644 4 US-10-282-112A-65644	12 US-10-282-122A-51957 12 US-10-282-122A-51957 12 US-10-282-122A-51957 15 US-10-369-493-13941 12 US-10-282-122A-59506
1361 1111 1111 1111 1111 1111 1111 1111	
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ALIGNMENTS

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Sequence 202680, Application US/10424599
Sequence 202680, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Can Vondwel
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202680
LENGTH: 94
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                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Clone ID: PAT_MRT3847_25044C.1.pep
US-10-424-599-202680
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Pred. No. 3.2;
2; Mismatches 3;
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Sequence 318, Application US/10043487

Publication No. US20030055220A1

GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
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31 TLDEMVHKRTLSPD 44
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.5
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max FEATURE:
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APPLICANT: PUSZTAI, LAJOS
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Shin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
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Pred. No. 5.1e+02;
3; Mismatches 5
                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NO 470
LENGTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 76, Application US/10092900A
Publication No. US20040043382A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li
APPLICANT: Carbusen, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1863 AIAVTVQEMVTKSNTSPE 1880
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rernandes, Elma R.
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Gangolli, Esha A.
Vernet, Corine A.M.
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55.6%;
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Catterton, Elina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guo, Xiaojia Sasha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alsobrook, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casman, Stacie J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malyankar, Uriel
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-177-293-470
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US-10-092-900A-76
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APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid
FILLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: 84778A
FILLE REFERENCE: 84778A
FILLE APPLICATION NUMBER: US/10/043,487
CURRENT FILLING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR APPLICATION NUMBER: US 60/261,130
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexmeri polypeptid
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexmeri polypeptid
TITLE OF INVENTION: Mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION WUMBER: US/10/043, 487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-0112
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
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     46.4%; Score 45; DB 14; Length 698;
1 Similarity 55.6%; Pred. No. 1.3e+02;
10; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 97;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-043-487-309
US-10-043-487-309
Sequence 309, Application US/10043487
PUBLICATION NO. US20030055220A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 470, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: CALORY, KAREN
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || |:|:| | ||||
|159 AIAVTVQEMVTKSNTSPE 176
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Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Shigella Flexneri
US-10-043-487-309
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Shigella Flexneri
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Wang, Youzhen
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Best Local Similarity
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                                                                                                                                                                                                                                                SEQ ID NO 318
LENGTH: 548
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LENGTH: 698
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APPLICANT:
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APPLICANT:
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PRIOR FILING DATE: 2003-02-0

PRIOR PEDILCATION NUMBER: 60/20,078

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-23

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-23

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-2-22

PRIOR PELING DATE: 2000-11-2-16

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-06

PRIOR PELING DATE: 2001-03-06

PRIOR PELING DATE: 2000-03-07

PRIOR PELING DATE: 200
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20
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44.3%; Score 43; DB
Best Local Similarity 44.4%; Pred. No. 31;
Matches 8; Conservative 7; Mismatches
                     1450 VAIKDLTLEELVDKRIGERNYEIRTDPE 1477
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Sequence.59186, Application US/10425114
GENERAL INFORMATION:
GAPPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kowin Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                 Sequence 53696, Application US/10282122A
Publication No. US20040029129A1
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58 SIKTTMREDVVEQILTPE 75
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                              JS-10-282-122A-53696
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APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Bieger, Daniel K.
TILE OF INTENTION: O. US200043382Alel Proteins and Nucleic Acids Encoding Same TILE OF INTENTION: N. US200043382Alel Proteins and Nucleic Acids Encoding Same TILE OF INTENTION: N. US200043004
CURRENT APPLICATION NUMBER: US5N 60/274,322
PRIOR PELLORION NUMBER: USSN 60/274,322
PRIOR PELLORION NUMBER: USSN 60/283,675
PRIOR PELLORION NUMBER: USSN 60/283,675
PRIOR PELLORION NUMBER: USSN 60/283,675
PRIOR PELLORION NUMBER: USSN 60/274,281
PRIOR PELLORION NUMBER: USSN 60/274,281
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR PELLORION NUMBER: USSN 60/279,995
PRIOR PELLORION NUMBER: USSN 60/294,899
PRIOR PELLORION NUMBER: USSN 60/294,424
PRIOR PELLORION NUMBER: USSN 60/294,424
PRIOR PELLORION NUMBER: USSN 60/294,424
PROME PELLORION NUMBER: USSN 60/294,424
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; Publication No. US20030233675A1
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR PILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; FEMALE OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.4%; Score 44; DB 12; Length 2545; Best Local Similarity 50.0%; Pred. No. 7.5e+02; Matches 9; Conservative 4; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 7.5e+02;
Mismatches 5;
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; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1867 AIAVTAQEMMTKSVTNPE 1884
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Best Local Similarity 50.0%;
Matches 14; Conservative
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2 VAIK-TTLKELVHKRV-----TSPE 20

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TYPE: PRT
ORGANISM: Caenorhabditis elegans
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674 VKNKLKELVEKKKTS 688
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  PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 6689 LENGTH: 1023
                                                                                                                                                                                                                                                                          4 IKTTLKELVHKRVTS 18
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Matches 9, Conservative
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                                                                                                                                                US-10-369-493-6689
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LENGTH: 29
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Jack Thua
APPLICANT: Screen, Steven E
APPLICANT: APACKE
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53113) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62723
LENGTH: 594
TYPE: ...
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59186
LENGTH: 594
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Pred. No. 2.2e+02;
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; OTHER INFORMATION: Clone ID: 700377412_FLI.pep
US-10-425-114-59186
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US-10-369-493-6689
Sequence 6689, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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50.0%;
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es 9; Conservative
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ORGANISM: Zea mays
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## PEDICANT: OBSOLOGICAL INFORMATION:
### APPLICANT: Cao, Yongwei
### APPLICANT: Cao, Yongwei
### APPLICANT: Slater, Steven C.
### APPLICANT: Slater, Steven C.
### APPLICANT: Goldman, Barry S.
### APPLICANT: Chen, Xianteng
### APPLICANT: Chen, Xianteng
### APPLICANT: UNFORTION: PLANTS WITH IMPROVED PROPERTIES
### TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
### TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
### CURRENT APPLICATION NUMBER: US/10/369,493
### CURRENT FILING DATE: 2003-02-28
### PRIOR FILING DATE: 2003-02-21
### PRIOR FILING DATE: 2003-02-21
### WUMBER OF SEQ ID NOS: 47374
### SEQ ID NO 6690
### ILENGTH: 1023
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Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT:
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US-10-424-599-174400
60/360,039
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; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Scre
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Indels
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US-10-425-114-62231
5,
Mismatches
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Publication No. US20040034888A1
GENERAL INFORMATION:
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172 LSIRRTARKLIHKRI 186
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8; Conservative
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILLE REFERENCE: 32-1(5323)B
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 254410
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Publication No. US20030068624A1

GENERAL INFORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific
TITLE OF INVENTION: Compositions and Proteins
TITLE OF INVENTION: Compositions and Proteins
FILE REFERENCE: DEX-0245
CURRENT APPLICATION NUMBER: 00/10/034,934
CURRENT FILING DATE: 2000-110-26
PRIOR PILING DATE: 2000-11-20
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                               Query Match 43.3%; Score 42; DB 12; Length 29; Best Local Similarity 44.4%; Pred. No. 12; Matches 8; Conservative 4; Mismatches 6; Indels
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US-10-424-599-254410
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; ORGANISM: Homo sapiens
US-10-034-934-116
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ORGANISM: Glycine max
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Perfect score:
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Mice minute virus Mice minute virus Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. AX137742 60 bp Sequence 7 from Patent BP1077260. AX137742 GI:14273915 RESULT 1
AX137742
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL

PAT 30-MAY-2001

linear

DNA

ALIGNMENTS

1 Nucesch,J. and Rommelaere,J. Parvovirus ns1 variants Patent: BP 1077260-A 7 21-FEB-2001; Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts

source

CDS

FEATURES

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Patent: EP 1077260-A 1 21-FEB-2001;
                                                                                                       Sequence 1 from Patent BP1077260. AX137736
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Patent: EP 1077260-A 8 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

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RESULT 2 AX137743 LOCUS DEFINITION

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ORIGIN

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Parvovirus ns1 variants
Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE) Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts $\langle \mathrm{DE} \rangle$ 60 1081 ACAAGAACCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. Mice minute virus Viruses; ssDNA viruses; Parvoviridae; Parvovirus 1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT Gaps Indels 0; 97.3%; Score 58.4; DB 6; Length 2019; 98.3%; Pred. No. 1.7e-09; ive 0; Mismatches 1; Indels 0 linear linear

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OTKKEVA I KTTLKELVHKR VTSPEDWMMQPDSY I EMMAQPGGENLLKNTLE I CTLTL
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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Parvovirus ns1 variants
Patent: EP 1077260-A 12 21-FBB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.3%; Score 58.4; DB 6; Length 2019; 98.3%; Pred. No. 1.7e-09; ive 0; Mismatches 1; Indels 0
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                                                                                                  note="unnamed protein product"
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                                                 'note="Parvovirus NS1 variant"
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/mol_type="unassigned DNA"
/db xref="taxon:10794"
/mol_type="unassigned DNA"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 from Patent EP1077260. AX137747
                                                                                                                                       /proteIn_id="CAC39991.1"
/db_xref="GI:14273914"
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                                                                                                                          /codon start=1
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Best Local Similarity 98.3
Matches 59; Conservative
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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AX137747
LOCUS
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/db_xref="REMTREMBL: CAC39997"
/taanslation="WAGNAYSDEVICATIVWLXEKSNQEVFSFVFKNENVQLNGKDIGW
NSYKKELQEDELKSLQEGETTWOGSEDMEWETTVUDEMTKKQVFIFDSLVKKCLFEVL
NTKNIFPGDVNWFVQBEWGROOGSHCHVLIGGKDFSQAQGKWWRRQLNVYWSRMLVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEBAĞNFĞQ
QVNQFKAIGSGQAIRIDQKGKGSKQIEPTPVIMTNRINITVRIGGESEPEHTQPIRD
RMLNIHITHTHEGPEGLVDKNEWPRI CAMLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPFPINLLGSARSPFTPKGTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucesch,J. and Rommelaere,J.
Barvovirus ns! variants
Patent: EP 1077260-A 16 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Minute virus of mice with two major open reading frames (genome).
V01115
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Mice minute virus
Mice minute virus
Viruses; seDNA viruses; Parvoviridae; Parvovirus.
1 (bases 1 to 5081)
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Length 2019;
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                                                Indels
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Score 58.4; DB 6;
Pred. No. 1.7e-09;
0; Mismatches 1;
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/note="unnamed protein product"
/codon_start=1
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                                                                                                                                                                                                                                                                                         DNA
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/organism="Mice minute virus"
/mol_type="unassigned DNA"
/db_xref="taxon:10794"
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Sequence 16 from Patent EP1077260.
AX137751
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1. .2019
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97.3%;
98.3%;
Query Match 97.3
Best Local Similarity 98.3
Matches 59; Conservative
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nes 59; Conserv
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/db_xref="GA1:04107"

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/td_xref="GA1:04107"

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MODITMAGNAYSDBYLAGATHWILKEKSNOEWFSFYKDRWYQLAGKDICHNSYKKELQB

DELKSLORGABTTWOSEDMEWETTVDEMTKKQVFIFDSLVKKCLFBYLATKNIFPGD

VNWFVQHEWGKDGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLYTACNVQLIFBE

RILKBRIDEBWYTLLTYKHKQTKQNYCYTKCVLFGNVATAYPTAGATSTSPPRDGGY

PLSSDSGWKTNFLKEGERHUVKKYTKOTKOTYCVLTAGFTATAGTSTSPPRDGGY

TTLKELVHKRVTSPEDWMMNQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
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IGSBASSPFTPRKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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SGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRDRMLNIHLTH
                                                                                                                                                                                                                                                                                                                                       is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion. Location/Qualifiers
                                                                                                                                                                                                                                          6298737
The messenger RNA of this virus (colinear with the strand listed)
Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
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/note="unnamed protein product; coding sequence"
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/note="unnamed protein product; coding sequence"
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                                                                                                                                                  Nucleic Acids Res. 11 (4), 999-1018 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mice minute virus"
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/db_xref="SPTREMBL:@89818"
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xref="SWISS-PROT:P03134"
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                                                     TITLE
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Vitying source taken induced with the control of th
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SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILI
NANPIGTKUDIHFSNVFNSYOSPLTAFERPSPVYDGOQAWDKELDLEHKRRLHITAPFV
CKNNAPGQMIVRLGPNITDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANITWNPV
YQVSAEDNGNSYMSVTKWLFTAIGNMQSVPLITRPVARNIY
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Statll,C.R., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5149)
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0
                                                                                                                                                                                                           Length 5081;
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JO2275 M12520 M12521 M14704
J02275. II GI:332293
alternative splicing; capsid protein; complete genome;
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                                                                                                                                                                                                Score 58.4; DB 14;
Pred. No. 1.7e-09;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5149 bp ss-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Three splicing patterns are used to to all minute virus of mice RNAs J. Virol. 60 (3), 1170-1174 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prototype strain
J. Virol. 57 (2), 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morgan, W.R. and Ward, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein.
Mice minute virus
Mice minute virus
                                                                                                                                                                                                           97.3%;
98.3%;
                                                                                                                                                                                                                                                                           59; Conservative
                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parvovirus
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AUTHORS
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COMMENT
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VERSION
KEYWORDS
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TITLE
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TITLE
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MEDLINE
PUBMED
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/translation="Mappakrakrgwvppgykylgpgnslddgeptwpsdaaakehde
AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEP
GSGVGRAGKRTRPPAYITNQARAKKLTSSAAQQSSQTMSDGTSQPDSGNAVAA
RVBRAAGPGCSGGGGGGGGGGYGTSYDNQTHYRPLGDGWVBITALATRLYHLNMP
KSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAMGVWLQPSDWQYICNT
                                                                                                                                                                                                                                                                                                                                                                                                                                    MSQLNI.VSLDQEI FNVVLKTVTEQDLGGGÄIKIYNNDLTACMMVAVDSNNILPYTPAA
MSMETLGFY WKPTI ASPYKYTKCVDNDLSVTTRENDGGTVEHVVMGTSKGNSQFFTI
NSTQQITLIRATGDERATGTYY POTNSVKLTHFWQTNRQLGQPPLLSTFPRADDAGTI
TAQGSRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFBASRAGPPAAPKVPADITQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKEANGSVRYSYGKOHGENWASHGPAPERYTWDETSFGSGRDTKDGFIOSAPLVVPPP
INGILINDANPTGTKNDIHFSNVFNSCOELTARENBSPYYGOGNWDKEEDLEHKRRLH
ITAFFVCKNNAPGOHLRLGEPULTDOYDPNGATLSRIVTYGTFFWKGKLTMRAKLRAN
TTWNPVYQVGAEDNGNSYMSVTKWLPTATGNMOSVPLITRPVARNTY"
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QVGFCQPHNDFEASRAGPFAAPKVPADITQGVDKEANGSVRYSYGKQHGENWASHGPA
PERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
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gsydnqthyrflgdgwveitalatrlvhlnmpksenycrirvhnttdtsvkgnmakdd
aheqiwtpwslvdanawgvwlqpsdwqyicntmsqlnlvsldqeifnvvlktvteqdl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="unknown protein"
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db_xref="GI:825482"
/translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                fnote="alternative intron"
join(2286. .2316,2399. .4557)
gene="VP1"
join(2286. .2316,2399. .4557)
gene="VP1"
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/db_xref="G1:825484"
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/db_xref="GI:825483"
/translation="MVGWWGINV"
2354. .2398
/gene="VP"
/note="RF2; putative"
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/db_xref="G1:332296"
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/gene="VP"
/note="VP intron (alt.)"
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/gene="VP"
/note="ORF3; putative"
/codon_start=1
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/gene="VP"
/note="ORF1; putative"
/codon_start=1
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/gene="VP1"
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/gene="VP1"
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SOLGTWAGNAXSDEVLGATWILKEKSNQEVPEKPRENVQLNGKDIGWISYKKELQE
DELKSLQRGAETTWDQSEDWEWETTVDEMTKKQVFIFDSLVKKCLFEVLANTKNIFPGD
VNWFVQHEWGKDQGAMTCHVLIGGKDFSQAQSKWWRRQLNVYWSRWLYTACNVQLTPAE
RIKLREIAEDNEWYTLLTYKHKQTKKDYTKCVLFGNMIAXYFLTKKKISTSFPRDGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product = "nonstructural protein"
/protein id="AAA67109.1"
/db_xref="d1:332295"
/translation="MAGNAYSDEVLGATWWLKEKSNOEVFSFVPKNENVQLNGKDIGW
/translation="MAGNAYSDEVLGATWPSETTYDEVTKKQVPIFDSLVKKCLFBVL
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NYSYKKRIPEPDVWWFVQHEWGROGWHFVVLIGGKDFSQAQCKWWRRQLAVYWSRWLVTA
CNVQLYPPAERIKLEARBARDNEWYTLLYKHKQYFKKDYFKCVLFGAMIAYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STGKSI I AQA I AQAVCHVGCYNAANVNPPFNDCTNKNL IWVEEAGNFGQQVNQFKA I C
SGQT IR I DQKGKGSKQI EPTPV IMTTNENI TVVR I GCEERPEHTQPI RDRMLNI HLTH
TLPGDFGLVDKNEWPMI CAWLVKNGYQSTWAS Y CAKWGKVPDWSENWAEPKVPTPI NL
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ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
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RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDMSENWAE
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
capsid proteins, VP1 (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2] revises [1].

[3] sites; splice sites.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10794"
/lab_host="mouse 1 (variant A-9) cell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="nonstructural protein"
/protein_id="AAA67108.1"
/db_xref="G1:825481"
                                                                                                                                                                                                                                        1. .5149
/organism="Mice minute virus"
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/gene="VP"
/note="alternative intron"
                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="MVM(p)"
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|gene="NS1"
|note="putative"
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/gene="VP"
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/gene="VP"
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/gene="VP"
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셤 ò

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ARTKTAFDLILEKAETSKLTNFSLPDTRTCKIFAFHGWNYVKVCHAICCVLNRQGGKR
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|gene="VP1"
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/gene="VP1"
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/gene="VPl"
/note="alternative intron"
2333. .2362
/gene="VPl"
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protein_id="AAA69568.1"
db_xref="GI:825478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="alternative intron"
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'protein_id="AAA69570.1"
'db_xref="GI:825479"
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'protein_id="AAA69569.1"
'db_xref="G1:332290"
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/codon_start=1
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/no+
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/gene="VP"
2003. .2281
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/gene="VP"
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/gene≃"VP"
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/gene="VP1"
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/gene="VP1"
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                                                                                    MVMICG 5085 bp 89-DNA linear VRL 05-JUL-1995 Minute virus of mice (MVM(i)), a lymphotropic variant of MVM, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Minute virus of mice (lymphotropic variant of MVM) DNA, clone pR0322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MISGSESLDQGAKRKWAWFKVYKQMLKSVTYPFFHSVSRDAQKE
SNQLTWAGNAYSDEVLGTTNWLKEKSNQEVFSFVFKTEDVQLNGKDIGWNNYKKELQE
DELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVFIYDSLVKKCLFEVLSTKNIAPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLPGDFGLŸDKNEWPMICAWLYKNGYOSTWASYCAKWGKVPDWSENWAEPKVPPTINS
LGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEBDLRACFGAEPLKRDFSEPLNLD"
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TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVFTTAQETKRGRI
OTKKEVSIKTTLKELVHKRVTSPEDWMMQPDSYIEMAAQPGGENLLKNTLEICTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTWPVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTACNVQLTPAE
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FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAOETKRGRIOTKKEVSIK
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STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQQVNQFKAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tränslation="MagnaySdEvLGTTNWLKEKSNQEVFSFVFKTEDVQLNGKDIGW
NNYKKELQEDELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVFIYDSLVKKCLFEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           mice,
                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. (Dases 1 to 5085)
Astell,C.R., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                               1 ACAAGAGCCTGCAGAATTTTTGCTTCATGGCTGGAACTATGTTAAAGTTTTGCCATGCT
                         Gaps
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                                                                                                                                                                                                                                                                                                               capsid protein; complete genome;
                       1; Indels
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protein_id="AAA69566.1"
db_xref="G1:825477"
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| Mol_Lype="genomic DNA"
| isolate="lymphotropic variant"
| db_xref="taxon:10794"
  Pred. No. 1.7e-09;
0; Mismatches 1
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/product="nonstructural_p
/protein_id="AAA69567.1"
/db_xref="GI:332291"
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1. .5085
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'gene="NS1"
'note="putative"
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                                                                                                                                                                                                                                                                                                             alternative splicing, on nonstructural protein.
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    98.3%;
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/gene="NS1"
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                         59; Conservative
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Mice minute virus
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Best Local Similarity
Matches 59; Conserv
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86115415
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NTVLFHGPASTGKSI I AQAI AQAVGNVGCYNAANVNFPFNDCTNKNLI WVEBAGNFGQ QVNQFKA I CSGQTI R I DQKGKGSKQ I EPTPV IMTTNEN I TVVR I GCEERPEHTQP I RD RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTMASYCAKWGKVPDWSENWAE PKVPTPINSLGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAE MSQLNLVSLDQEI FNVVLKTVTEQDSGGQÄI KI YNNDLTACMMVAVDŠNNI LPYTPAA NSMETLGFY PWKPT I ASPYRYYFCVDRDLSVTYENQEGT I EHNVMGTPKGMNSQFFT I DREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPP LNGI LTNANPI GTKNDI HFSNVFNSY QPLTAFSHPSPVY PQGQI WDKELDLEHKPRLH I TAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRI VTY GTFFWKGKLTMRAKLRAN translation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE" ENTQQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTL AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEP TAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGV **TONTGEAGSKACODGOLSPTWSEIEEDLRACFGAEPLKRDFSEPLNLD** ITWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY" note="minor transcription start site" number=1 note="major transcription start site" note="minor transcription start site"

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HOU34255
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1 (bases 1 to 5087)
Sahli,R., McMaster,G.K. and Hirt,B.
DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
                                                                                                                                                                                                                                                                                                  AHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQDS
GQAAIKIYNDDLTACMWYDNDSNNILPYTPAAANSMETLGFYFWKFTIAEBPYRYFEVD
RDLSVTYENOBGTIENTWMGTPKGMNSQPFTIENTQDITLLRTGDEFATGTYYFDTND
VKLITHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPA
                                                                                                                                                                                                                                                                                                                                                                                QVGFCQPHNDFEASRACPFAAPKVPADVTGGVDREANGSVRYSYGKQHGENWAAHGPA
BERYTWDETRFGSGROTRDGFTQGSPLVVPPENGILTWANDFGTKNDHFBSNFNSY
GPLFARSHPSSPVYGQGJUNDKELDLEHKPRLHTAPPVCKNNAPGGMLVRLGPBLTDG
YDPNGATLSRIVYTGTFFWKGKLITMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAMVMI 5087 bp DNA linear VRL 01-JUL-1999 Mouse parvovirus minute virus immunosuppressive variant genome ( =
                                                                                                                                                                                                                                                          /translation="MSDGTSQPDGGNAVHSAARVERAADGPGGSGGGGSGGGGGVGVST
GSYDNQTHYRPLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For the fibroblast-specific strain (MVMp) sequence see <PAMVM2>. The genomes of MVMp and MVMi (immunosuppressive variant) have more than 96% of their sequence in common.

Data kindly reviewed (18-JUL-1986) by G. McMaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coat protein; genome; origin of replication; overlapping genes; terminal repeat; unidentified reading frame. Mice minute virus Mice minute virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 92.0%; Score 55.2; DB 14; Length 5085; 1 Similarity 95.0%; Pred. No. 2.1e-08; 57; Conservative 0; Mismatches 3; Indels 0;
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/organism="Mice minute virus"
/organism="Mice minute virus"
/mol type="genomic DNA"
/db xref="taxon:10794"
1. :116
/note="terminal hairpin region"
                  db_xref="GI:825480"
/translation="MFNYLFYRPEITWF"
                                                                                                                                                                                                  /codon_start=1
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/db_xref="G1:332292"
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protein_id="AAA69571.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1085 bp updstream of EcoRI site.
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/note="TATA box"
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/gene="VP1"
<2405. .4558
/gene="VP1"
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/gene="VP2"
2795. .4558
/gene="VP2"
                                                        2400. .>4558
/gene="VP1"
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                                                                                                                                                            CDS
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SGGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSWETLGFYPWKPTIASPYRYYFCV
DRDLSYYTEWDGGTISHNYMGTPKGMNSQFFTIENTQOITLLATGDEPATGTYYFDTN
PVKLTHTWQTNRQLGQPPLLSTPPEADTDAGTLTAGGSRHGATQMSWNWVSRAIRFR
AQVGFCOPHNDPEASRAGPPAAPKVPADVTQGVDREANGSVRYSYGKQHGENMAAHGP
APERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="VP2 protein"
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/protein_id="CAB46508.1"
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/db_xref="SWISS-PROT:P07302"
/tb_xref="WPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDQYIKSGKNP
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QYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
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Viruses, soDNA viruses, Parvoviridae, Parvoviruses, soDNA viruses, Parvovirus.
1 (bases 1 to 4773)
1 (bases 1 to 4773)
1 (bases 1 to 4773)
1 (bases 2 to 4773)
1 (bases 3 to 4773)
1 (bases 4 to 4773)
1 (bases 4 to 4773)
1 (bases 4 to 4773)
2 (bases 4773)
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2 (bases 4773)
3 (bases 4773)
4 (bases 4773)
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6 (bases 4773)
6 (bases 4773)
6 (bases 4773)
7 (bases 4773)
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/note="polyadenylation signal"
4821. .4826
/note="polyadenylation signal"
4878. .5087
/note="terminal hairpin region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%; Score 55.2; DB 14;
95.0%; Pred. No. 2.1e-08;
ive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="coat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTATGNMQSVPLITRPVARNTY"
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/gene="VP2"
<2792. .4558
/gene="VP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U34255.1 GI:1464792
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ORIGIN

FEATURES

AUTHORS TITLE JOURNAL

PUBMED

REFERENCE

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1202 ACAAGAACCTGCAAGATCTTTGCTTTTCATGGCTGGAACTACATTAAAGTTTGCCATGCT 1261
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Mouse parvovirus 1c
Viruses; sebNR viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (Dases 1 to 4764)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
96201434
             Viruses; sSDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases 1 to 4764)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L., Franklin, C.L., Hook, R.B. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Submitted (17-AUG-1995) David G. Besselsen, Department (Veterinary Pathology, University of Missouri-Columbia, Veterinary Medicine Building, Columbia, MO 65211, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

84.0%; Score 50.4; DB 14; Length 4764;
Best Local Similarity 90.0%; Pred. No. 9.3e-07;
Matches 54; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                     Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department
Veterinary Pathology, University of Missouri-Columbia,
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.4; DB 14;
Pred. No. 9.3e-07;
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/organism="Mouse parvovirus lb"
/mol_type="genomic DNA"
/specific_host="Mus musculus"
/db_xref="teaxon:42841"
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/specific host="Mus musculus"
/db_xref="taxon:42842"
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U34254
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90.0%;
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Besselsen, D.G.
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  Mouse parvovirus 1b
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Best Local Similarity
Matches 54; Conservat
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  ORGANISM
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Viruses; SBDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (Dases 1 to 4761)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L., Franklin, C.L., Hock, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
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                                                           Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Bullding, Columbia, MO 65211, USA
Location/Qualifiers
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Submitted (17-AUG-1995) David G. Besselsen, Department
Veterinary Pathology, University of Missouri-Columbia,
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   Length 4773;
                                                                                                                                                                                                                                                                                                                                Score 52; DB 14; Length 47
Pred. No. 2.6e-07;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                              /organism="Hamster parvovirus"
|mol_type="genomic DNA"
/specific host="Mesocricetus auratus"
|db_xref="taxon:42843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /specific_host="Mesocricetus auratus"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4761 bp
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U34253
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Conservative 0;
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Mice minute virus DNA.
U34256
                    2 (bases 1 to 4773)
Besselsen, D.G.
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Besselsen, D.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mice minute virus
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Best Local Similarity
Matches 55; Conserv
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8609486
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ORGANISM

SOURCE

AUTHORS

REFERENCE

TITLE JOURNAL MEDLINE

REFERENCE AUTHORS TITLE JOURNAL

DEFINITION

WVU34256

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ACCESSION

VERSION KEYWORDS

VRL 21-AUG-1996

Gaps

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RESULT 15

Mouse parvovirus 1b

RESULT 13
MOU34253
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

source

FEATURES

Best Loca Matches

ORIGIN

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MPU12469 S144 bp DNA linear VRL 24-JAN-1995 Mouse parvovirus 1 complete genome, nonstructural protein 1 (NS1) gene, complete cds and capsid protein (VP1) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPPROGGERICAL SCRUGGERIL VERGERHLIVSKLYTDDRRPETTETTYTTAGETKRRRI OTKKEVSIKTIKELVHKRYTSPEDWYMMOPDSYIEMYAQPGGENLLKNTLEICTLTL ARTKRAPDLILEKAETGKLTNFBLPDTRTCKIFAFHGMYTKYTHADCTUNRQGGKR NATVEHGBASTGKSIIAQAAQVGANAANVEPFNDCTNKNLIWVEBAGNFGQ OVNOFKAICSGOTTIR 100KGKOSKQIEPTPVIMTUNBYTVKIGCERPEHTOPIND RMLNIHLIHTLPGDFGLVDDKNEWPINICAMLVKNGYQSTWASYCAKWGKVPDWTENWAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTÔRI OLLRYGDEFATGTYYFETEPIKLSHTWOSNRQLGQPPQI TDLPTADNENATLV
TRGDRSGI TQI SGSNDVTEATRVRPAQVGFCQPHDNFETSRAGPFKVPVVPANVTQGN
EHDANGSLRYTYDKQHQDWGSNNSKERFTWDA I SYDSCRWADRCFINATPFTSPPAL
NNI LTNSDPI GNKTA IHYGNSYGPLTAFPHPAPI Y PQGQTWDKELDLEHKRLHA
QAPFVCKNNAPGQLI-VRLAPNI TDQYDPNSSTLSRI VTYYGTFFWKGKLTLKAKLRPNA
TWNPVYQVSAQYQNENEYMSI HKWLPTATGNMQSI PLLSRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVERAADGPGGGGGGGGGGGGGGGGGGGTRARAHLMMP
KSENYCRVRVHNTNDTRTAGNMAKDDAHEQIWTPWSLIDSNAMGVWFQPSDWQFICNN
MSHVNLHSLDQELFNVVIKTVTEQNTGAEAVKIYNNDLTASMMVALDSNNILPYTPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNYKKELQEDELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVFIYDSLVKKCLFEVL
STKNIAPADVTWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNVQLTPAERIKLREIAEDSEWVTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTSGVSI AGKRTKPPAHI FINQARAKKRASLAAQQRTQTMSDGAEQPDSGSAVQSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MagnaySDBVLGTTNWLKEKSNQEVFSFVFKTEDVQLNGKDIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDF
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                                                                                                                                                                 Mouse parvovirus 1
Mouse parvovirus 1
Mouse sarvovirus 1
Mouses; saDNA viruses; Parvoviridae; Parvovirus.
1 (bases 1 to 5144)
Ball-Goodrich, L. J. and Johnson, E.
Molecular characterization of a newly recognized mouse parvovirus J. Virol. 68 (10), 6476-6486 (1994)
94365951
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ball-Goodrich, L.J.
Direct Submission
Submitted (20-JUL-1994) Lisa J. Ball-Goodrich, Section of
Comparative Medicine, Yale University School of Medicine, New
Haven, CT 06520-8016, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 .5144
/organism="Mouse parvovirus 1"
/mol_we="genomic DNA"
/db_xref="taxon:55340"
/clone="pRVXB36; pLTB/RI3-6; pRTBg/H3-1"
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/product="nonstructural_protein 1"
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/gene="NS1"
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MPU12469
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84.0%; Score 50.4; DB 14; Length 5144; 90.0%; Pred. No. 9.3e-07;

Query Match Best Local Similarity

ORIGIN

Search completed: June 2, 2004, 18:58:36 Job time : 653 secs

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2, 2004, 15:24:48; Search time 145.25 Seconds (without alignments) 1754.849 Million cell updates/sec
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                                                                                                                                                                                        US-10-069-056-7
60
1 acaagagcctgcagaatttt......atgttaaagtttgccatgct
                                                                                                                                                                                                                                                                                                                                                                     6747726
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               3373863 segs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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	Description	Aad02800 Parvoviru	Aad02801 Parvoviru	Aad02805 Parvoviru	Aad02803 Parvoviru	Aad02797 Parvoviru	Aad02799 Parvoviru	Aan40252 Sequence	Aat15311 Non-atten	Aat15312 Attenuate	Aat88321 Attenuate	Aat88324 Attenuate	Aat88320 Canine pa	Continuation (4 of	Aaz01425 Complete	Aaf94965 Human ova	Abl48915 Ovarian c	Abt03232 Human ova	Adc86554 Human GPC	Aah51601 Human chr	Aas09301 Human sch	Aad34050 Chicken D	Abl17874 Drosophil	Aak68375 Human imm
SUMMARIES	ID	AAD02800	AAD02801	AAD02805	AAD02803	AAD02797	AAD02799	AAN40252	AAT15311	AAT15312	AAT88321	AAT88324	AAT88320	ADE11169 3	AAZ01425 00	AAF94965	ABL48915	ABT03232	ADC86554	AAH51601	AAS09301	AAD34050	ABL17874	AAK68375
	Length DB	9 09	2019 5	2019 5	2019 5	2019 5	2019 5	3524 1	5049 2	5049 2	5049 2	5049 2	5049 2	94191 9	110000 2	396 4	396	396	113306 9	319608 3	319608 5	4545 6	2654 4	10280 4
	% Query Match	100.0	100.0	97.3	97.3	97.3	97.3	52.0	47.7	47.7	47.7	47.7	47.7	44.7	44.3	42.7	42.7	42.7	42.7	42.7	42.7	42.3	42.0	41.3
	Score	09	9	58.4	58.4	58.4	58.4	31.2	28.6	28.6	28.6	28.6	28.6	26.8	26.6	25.6	25.6	25.6	25.6	25.6	25.6	25.4	25.2	24.8
	Result No.		7	m	4	Ŋ	9	7	œ	σ	. 10	11	12	c 13	14	15	.16	17	c 18	19	20	c 21	c 22	c 23

Abz35015 Human gen	Aak98324 Human pur	Aak75098 Human imm	Aahl0099 Human cDN	Adb57189 Toxicity-	Abz16033 Arabidops	Aah15544 Human cDN	Abv53447 Human pro	Abv51185 Human pro	Abn67977 Streptoco	Ada32213 DNA encod	Aai59218 Human pol	Aah04336 Human cDN	Aaf29474 Mouse TAN	Aaf29491 Mouse TAN	Aaf29490 Mouse TAN	Aaf29489 Mouse TAN	Abx17941 Glycoprot	Abx17939 Glycoprot	Abx17924 Mouse TAN	Abx17940 Glycoprot	Aaf29473 Mouse TAN
ABZ35015	AAK98324	AAK75098	AAH10099	ADB57189	ABZ16033	AAH15544	ABV53447	ABV51185	ABN67977	ADA32213	AAI59218	AAH04336	AAF29474	AAF29491	AAF29490	AAF29489	ABX17941	ABX17939	ABX17924	ABX17940	AAF29473
9	9	4	4	0	9	4	Ŋ	Ŋ	9	œ	4	4	4	4	4	4	7	7	7	7	4
136328	9905	20752	559	642	2000	2996	593	595	846	861	876	897	939	939	939	939	939	939	939	939	1163
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24.8	24.6	24.4	24	24	24	24	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8
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ALIGNMENTS

/partial replace(7, A) / tage B / trage B / trage B / hocation corresponds to position 1087 of the NSI variant (T363A) DNA shown in AAD02801" Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity. NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds. Parvovirus non-structure protein 1 (NS1) variant (T363A) DNA fragment. /*tag= a
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/note= "CDS does not include start and stop codon" (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. Location/Qualifiers AAD02800 standard; DNA; 60 BP. 99EP-00115161. 99EP-00115161. (first entry) Rommelaere J; (revised) WPI; 2001-212717/22. P-PSDB; AAY72705. 13-AUG-1999; 13-AUG-1999; 06-AUG-2003 31-MAY-2001 EP1077260-A1 21-FEB-2001. Parvovirus. Nueesch J, Synthetic. AAD02800; mutation RESULT 1 AAD02800 Key

therapy. (Updated on 06-AUG-2003 to correct OS field.)

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The present sequence is a parvovirus non-structure protein 1 (NS1) variant (TS45A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxidity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as toxins for treating therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                        NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                          1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                   ;
0
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                                                                                                                                                                      100.0%; Score 60; DB 5; Length 60; 100.0%; Pred. No. 5.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
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replace(1187, A)
/*tag= b
                                                                                                                                            Sequence 60 BP; 15 A; 11 C; 13 G; 21 T; 0 U; 0 Other;
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1. .2019
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             Disclosure; Page 16; 41pp; English.
                                                                                                                                                                                                                                                                                                                   AAD02801 standard; DNA; 2019 BP
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31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1077260-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
                                                                                                                       1 ACAAGAGCCTGCAGAATTTTTGCTTTTTCATGGCTGGAACTATGTTAAAGTTTTGCCATGCT
                                                                                            Gaps
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                                                              Length 2019;
                              Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "NS1 variant (T463A) protein"
                                                          100.0%; Score 60; DB 5; L
100.0%; Pred. No. 1.2e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a /product= "NS1 varreplace(1387, A) /*tag= b
                                                                                                                                                                                                                             AAD02805 standard; DNA; 2019 BP
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                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                    Query Match
Best Local Similarity 100./
Matches 60, Conservative
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                 Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                             AAD02805;
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Best Local S:
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                             RESULT 3
SXX
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1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGCTGGAACTATGTTAAAGTTTGCCATGCT 60

The present sequence is a DNA encoding parvovirus non-structure protein (NS1) variant (T363A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cyclocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene

Claim 7; Page 16-19; 41pp; English.

NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; ds.

/*tag= a /product= "Parvovirus NS1 protein"

Location/Qualifiers 1. .2019

Parvovirus

Key

Parvovirus non-structure protein 1 (NS1) wild-type DNA

(revised)
(first entry)

06-AUG-2003 31-MAY-2001

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g
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1081 ACAAGAACCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a DNA encoding parvovirus non-structure protein (NSI) variant (T394A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58.4; DB 5; Length 2019;
Pred. No. 4.4e-11;
0; Mismatches 1; Indels 0.
                                                                                                                                 Parvovirus non-structure protein 1 (NS1) variant (T394A) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  /*tag= a
/product= "NSI variant (T394A) protein"
replace(1180, A)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                  KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 22-24; 41pp; English
                                                            ВР
                                                           AAD02803 standard; DNA; 2019
                                                                                                                                                                                                                                                                                                                            99EP-00115161
                                                                                                                                                                                                                                                                                                                                                99EP-00115161
                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                        .2019
                                                                                                                                                                                                                                                                                                                                                                                       Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-212717/22
                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY72708
                                                                                                                                                                                                                                                                                                                                                                  (DEKR-) DEUT
                                                                                                                                                                                                                                                                                     EP1077260-A1
                                                                                                                                                                                                                                                                                                                             13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                13-AUG-1999;
                                                                                                  06-AUG-2003
31-MAY-2001
                                                                                                                                                                                                                                                                                                        21-FEB-2001.
                                                                                                                                                                                  Parvovirus
                                                                                                                                                                                           Synthetic.
                                                                               AAD02803;
                                                                                                                                                                                                                                                       mutation
                                                 RESULT
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Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

Disclosure; Fig 1; 41pp; English

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM

Nueesch J, Rommelaere J; WPI; 2001-212717/22. P-PSDB; AAY72702.

99EP-00115161. 99EP-00115161

13-AUG-1999; 13-AUG-1999;

EP1077260-A1

21-FEB-2001

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1140
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The present sequence is a wild type DNA encoding parvovirus non-
structure protein 1 (NS1). The present invention relates to the variants
of the parvovirus non-structure protein (NS1) having a shifted
equilibrium between the DNA replication and transcription activities, and
the cytotoxicity activity. These variants are useful as toxins for
treating tumoural diseases. The variant DNAs are useful as vectors for
gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
                                                                                                                                                                                                                                                                                                                                                                          1081 ACAAGAACCTGCAGAATTTTTGCTTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                            1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                             Query Match 97.3%; Score 58.4; DB 5; Length 2019; Best Local Similarity 98.3%; Pred. No. 4.4e-11; Matches 59; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA
                                                                                                                                                                                                  Sequence 2019 BP; 698 A; 389 C; 452 G; 480 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD02799 standard; DNA; 2019 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
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31-MAY-2001
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Synthetic.
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Gaps ö

1; Indels

97.3%;

Local Similarity 98.3 Les 59, Conservative

Query Match Best Local S

Matches

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1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60

AAD02797 standard; DNA; 2019 BP

RESULT 5
AAD02797
ID AAD0
XX
AC AAD0

AAD02797

Location/Qualifiers

.2019

Key

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM

Nueesch J, Rommelaere J;

WPI; 2001-212717/22. P-PSDB; AAY72704.

99EP-00115161

13-AUG-1999; 13-AUG-1999;

EP1077260-A1

mutation

21-FEB-2001

99EP-00115161

Claim 7; Page 11-14; 41pp; English

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1084 ACAAGAACATGTAAAATATTCAGCATGCACAATTGGAACTACATTAAAGTCTGCCATGCT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relative to control
disease in animals,
                                                                                                                                                                                                                                                         Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                 The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This viral DNA is isolated from a non- attenuated CPV. The DNA is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match S2.0%; Score 31.2; DB 1; Length 3524; Local Similarity 70.0%; Pred. No. 0.32; les 42; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3524 BP; 1400 A; 719 C; 648 G; 757 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-attenuated canine parvovirus CPV-39 passage 5 DNA.
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CPV
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                                                                                                                                                                                                                                                                                                                  Claim 10; Table II, Page 33-49; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gruenberg A, Carmichael LE;
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                                                                     83US-00459203
84US-00567968
                                    84WO-US000063
                                                                                                                                                                                                     WPI; 1984-201354/32.
P-PSDB; AAP40306, AAP40675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine parvovirus
                                                                                                                               (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9614088-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1995;
                                    19-JAN-1984;
                                                                         19-JAN-1983;
06-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-0CT-1996
02-AUG-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT15311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                  Fox GM;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 ACAAGAACCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a DNA encoding parvovirus non-structure 1 protein (NS1) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                               Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein envelope; immunogen; vaccine; antigen; epitope; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                        /*tag= a /*tag= n/fproduct= "NS1 variant (S283A) protein" replace(647, A) /*tag= b /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58.4; DB 5;
Pred. No. 4.4e-11;
0; Mismatches 1;
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Porcine parvovirus; NADL-2 virulent strain

AAN40252 standard; DNA; 3524 BP

(first entry)

(revised)

24-OCT-2003 12-JAN-1992

AAN40252;

parvovirus

97.3%; 98.3%;

59; Conservative

Matches

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Local Similarity

Query Match

Location/Qualifiers

.2073

/*tag= b /note= "see AAP40675" /*tag= a /note= "see AAP40306" 2107. .3522

WO8402847-A.

CDS

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Gaps

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Gaps

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Indels

19; DB 2;

Score 28.6; DB Pred. No. 3; 0; Mismatches

Length 5049;

9

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1357 CTAGAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                  2 CAAGAGCCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                             parvovirus; CPV; attenuation; vaccine; dog;
panleukopenia virus; mink enteritis virus; infection; ds
   Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                             Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                AAT88321 standard; DNA; 5049 BP
                                 ch 47.7%;
1 Similarity 67.8%;
40; Conservative
                                                                                                                                                                                                                                                                              (first entry)
                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Canine parvovirus.
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                                                                                                                                                                                                                                                                              21-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                            feline
                                                                  Matches
                                                                                                                                                                                RESULT 10
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preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEMSZ. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vBI440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEN3Z or pGEN5Z. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                               2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                         Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                                                                                                                                                   Gaps
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                                                                                                  Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                  Length 5049;
                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Attenuated canine parvovirus CPV-39 passage 60 DNA
                                                                                                                                Score 28.6; DB 2;
Pred. No. 3;
                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parrish CR, Gruenberg A, Carmichael LE;
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"A, С с
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                                                                                                                                  47.7%;
67.8%;
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                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1996
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                                                                                                                                                                                                                             1357
                                                                                                                                   Query Match
                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                            RESULT 9
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(G in passage

/*tag= c /note= "base 4307 is A in virulent CPV-39 65 attenuated virus)"

coding region"

Location/Qualifiers *tag= a note= "NS1/NS2 coding region'

'note = "VP1/VP2

*tag=

.4541

passage

금

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in virulent CPV-39

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Canine parvovirus DNA carrying specific attenuating mutation(s) - used as
                                                            (A in passage
                                                                                                    passage
                                                                                                                                             passage
                                                                                                                                                                          /*tag= h
/note= "base 4973 is C in virulent CPV-39 (T in passage
65 attenuated virus)"
                                                                                                   (T in
                                                                                                                                            (T in
                                               /*tag= e
/note= "base 4409 is C in virulent CPV-39
65 attenuated virus)"
                                                                       /*tag= f
/note= "base 4477 is G in virulent CPV-39
65 attenuated virus)"
4889
                                                                                                                                   g
"base 4889 is C in virulent CPV-39
                                                                                                                                                                                                                                                                                                                        Gruenberg A;
/*tag= d
/note= "base 4358 is C in
65 attenuated virus)"
4409
                                                                                                                                                      65 attenuated virus) "
                                                                                                                                                                                                                                                                                                   (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                            97WO-US007584
                                                                                                                                                                                                                                                                                                                        Carmichael LE,
                                                                                                                                     *tag=
                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                            WPI; 1998-008583/01
                                                                                                                                                                                                                                                                                                                        Parrish CR,
                                                                                                     FFFFFFFFFXXX6X4X4X4X1X4XF
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us-10-069-056-7.rng

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trendated viruses are obtained by serial passage of the viruleme.

type 2b isolate 39 in NLFK feline kidney host cells. They have one or more of the sequence alterations indicated in the sequence relative to the sequence of a control (5th passage) wild-type CPV-2b (see AAT88320).

A claimed virus from the 65th passage) wild-type CPV-2b (see AAT88320).

A claimed virus from the 65th passage (deposited as ATCC VR 2528)

C contains all 6 mutations. The DNA from attenuated CPV strains (see also AAT88324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response.

(NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1357 CTACAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
for protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= d
note= "base 97 is C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parvovirus; CPV; attenuation; vB1440; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                Sequence 5049 BP; 1788 A; 809 C; 1029 G; 1417 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= e
note= "base 4745 is T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= f
/note= "base 4881 is C in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/note= "base 59 is G in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated canine parvovirus (vBI440) genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                Score 28.6; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= a
note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canine parvovirus; vBI440 (ATCC VR 2489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT88324 standard; DNA; 5049 BP.
                                               Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                              67.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 67.8
nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                  virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9742972-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2003
21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT88324;
   vaccines
                                                                                This DNA
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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passaging (60 times) of virulent canine parvoirus (CPV) type 2b isolate 39 in NLFK feline kidney host cells. The attenuated virus is designated 39 in NLFK feline kidney host cells. The attenuated virus is designated (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations are within the hairpin formed by the 3' terminal palindrome: the mutation at uncleotide 59 introduces an A into a G-C rich region within the tip of the hairpin, disrupting the base pairing in one of the 2 small internal palindromes within the palindromes within the palindrome. The DNA from attenuated CPV strains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the against CPV disease, or more generally in cats and minks to protect against feline panleukopenia virus and mink enteritis virus. The vaccines contect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response.
                                                                                                                                                                   Canine parvovirus DNA carrying specific attenuating mutation(8) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1357 CTAGAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                                                                                                                                                                                                DNA sequence comprises an attenuated virus genome derived by serial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CAAGAGCCTGCAGAATTTTTTTTTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parvovirus, CPV, attenuation, vB1440, vaccine, dog,
panleukopenia virus, mink enteritis virus, infection, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.7%; Score 28.6; DB 2; Length 5049; 67.8%; Pred. No. 3; 11ve 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
273. .2279
/*tag= a
/note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine parvovirus 39 passage #5 (wild-type).
                                                                                                     Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canine parvovirus; type 2b isolate 39
                                                                                                                                                                                                                                             Example 8; Page 34-37; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT88320 standard; DNA; 5049 BP
                                                                    (CORR ) CORNELL RES FOUND INC
97WO-US007584.
                                  96US-00647655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 67.8 (es 40; Conservative
06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9742972-A1.
                                  15-MAY-1996;
                                                                                                       Parrish CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2003
21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT88320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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8
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The present sequence represents the complete genome of Chlamydia trachomatis. Open reading frames (ORPS) of the genome encode polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to control growth of the microorganism. Chiamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38590 AGAGCATGTAGATCTTTTACGAGTAGGGCTCGCAATATGCAAAATTTTGTCTTGCT 38646
                                                                                                                                                                                                                                                           Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genical disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1038602 BP; 304265A; 214645C; 214259G; 305001T; 0U; 432Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AGAGCCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                         Complete genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26.6; DB 2;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 373-656; 1755pp; English
                 710000
810000
910000
1010000
                                                                                         AAZ01425_10 1000001 10386
AAZ01425 8tandard; DNA; 1038602 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97FR-00015041.
97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-IB001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF94965 standard; cDNA; 396
                 600001
700001
800001
                                                                       900001
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-371125/31.
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es 38; Conserv
                 AAZ01425_06
AAZ01425_07
AAZ01425_08
AAZ01425_09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
AAZ01425 05
                                                                                                                                                                                                                                                                                                                                                                                             WO9928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1998;
                                                                                                                                                                                      17-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffais R;
                                                                                                                                                   AAZ01425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF94965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ID AAF9
XX
AC AAF9
XX
DT 23-M
g
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Continuation (4 of 4) of ADE11169 from base 300001 (Human transporter protein encoding
WP Sequence split into 4 fragments LoCUS ADE11169 Accession Ade11169
WP Fragment Name Begin End
WP ADE11169 1 100000 1 100000
WP ADE11169 2 200001 310000
WP ADE11169 3 300001 394191
                                                                                                                                                                                                                                                                                                                             This DNA sequence comprises the genome of virulent canine parvovirus type 2D (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline kidney host cells. Purther passaging has yielded attenuated virus wB1440 (APCC VR 2489) (see AAT88324) from the 60th passage, and a claimed virus C see AAT88321) derived from the 65th passage (APCC 2528). These cespectively contain 4 and 6 mutations in comparison to the virulent 5th passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against CPV disease, or more generally in cats and minks to protect against felline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), and provide a long term immune response. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                       Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1357 CTAGAACATGTCAAATTTTTAGAATGCACGGATGGAATTGGATTAAAGTTTGTCACGCT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42939 GAGCATGTAAAATTTTCTTTTCTACTTAGTGGAAAACTGTTAAAGTTTGCTAAG 42886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS AAZ01425 Accession Aaz01425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 94191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.6; DB; Pred. No. 3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 25;
0; Mismatches
                                                                                                                                                 Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26.8;
Pred. No. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310000
410000
510000
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                                                                                                                                                                                                                                                                                                Example 8; Page 37-40; 60pp; English
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                                  97WO-US007584
                                                                       96US-00647655
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es 37; Conservative
                                                                                                                                                                                    WPI; 1998-008583/01
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                                    06-MAY-1997;
                                                                       15-MAY-1996;
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Matches

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Best Loc Matches

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Search completed: June 2, 2004, 19:08:30 Job time : 149.25 secs

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Gaps

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Ouery Match 42.7%; Score 25.6; DB 4; Length 396; Best Local Similarity 63.8%; Pred. No. 21; Matches 37; Conservative 0; Mismatches 21; Indels (

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2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
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Best Local Similarity
Matches 40; Conserv
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ORGANISM: Pai
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Sequence 156, App
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Sequence 2, Appli
Sequence 1, Appli
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1016.704 Million cell updates/sec
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                                                                     2, 2004, 18:58:44 ; Search time 32.75 Seconds
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'Gqn2 6/ptodata2/ina/5A_COMB.seq:*
'Gqn2 6/ptodata2/ina/5B_COMB.seq:*
'Gqn2 6/ptodata2/ina/6A_COMB.seq:*
'Gqn2 6/ptodata2/ina/6B_COMB.seq:*
'Gqn2 6/ptodata2/ina/PCTUS COMB.seq:*
'Cqn2 6/ptodata2/ina/PCTUS COMB.seq:*
'Gqn2 6/ptodata/2/ina/PCTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-09-621-976-9809
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                                                                                                                                                                                                     682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                               nucleic search, using sw model
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seq length: 200000000
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Match Length DB
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1284, Ap
463, App
29, Appl
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
ATTLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NY
ZIP: 10036-2711
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
                                        US-09-107-532A-1284
US-09-107-532A-463
US-09-207-565-29
US-08-365-981-5
US-09-480-884A-151
US-09-480-884A-151
US-09-66-421B-151
US-09-60-421B-151
                     US-09-134-000C-1283
US-09-287-599A-7
                                                                                                                                                                              US-08-961-527-210
US-09-134-000C-2759
                                                                                                                                             US-08-306-691B-21
US-09-023-655-1335
                                                                                                                                                                     PCT-US93-06251-25
                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30753
7937-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 30753
TELECOMMUNICATION INPORMATION:
TELEPAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08336345 Patent No. 5814510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                     1038
1128
2070
2070
915
1087
4655
4655
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5084
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11378
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Gaps

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Score 28.6; DB 1; Length 5049; Pred. No. 0.37; 0; Mismatches 19; Indels 0

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Patent No. 5814510

GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gruenchael, Leland B.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.7%; Score 28.6; DB 1; Length 5049; Best Local Similarity 67.8%; Pred. No. 0.37; Matches 40; Conservative 0; Mismatches 19; Indels 0
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US-08-647-655-1

Sequence 1, Application US/08647655

Patent No. 5865585

GENERAL INFORMATION:

APPLICANT: Parrish, Colin R.

APPLICANT: Carmichael, Leland E.

TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: 3

CORRESPONDENCE ADDRESS: 4

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NY
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
FILING DATE:
CLASSIFICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: GOTGON, Jennifer
REGISTRATION NUMBER: 30753
REPERBNCE/CATION INFORMATION:
TELECOMMUNICATION INF
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ORGANISM: Parvovirus
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STRANDEDNESS: both
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HYPOTHETICAL: NO
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MURDITURES APPLICATION NUMBER:

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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.484C4
CURRENT APPLICATION NUMBER: US/09/713,550
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 205
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                               19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                Score 28.6; DB 2;
Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                               0; Mismatches
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US-09-713-550-156
; Sequence 156, Application US/09713550
; Patent No. 6617109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 156, Application US/09640173 Patent No. 6613515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NAME/KEY: misc_feature
| LOCATION: (1)...(396)
| OTHER INFORMATION: n = A,T,C or G
US-09-640-173-156
                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                             Query Match 47.7%;
Best Local Similarity 67.8%;
Matches 40; Conservative (
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                         unknown
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-640-173-156
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LENGTH: 396
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##PAPLICANT: BAIDAIN, DELHABLA,
##PAPLICANT: BAIDAIN, BERIOUX, LAURENT
##PAPLICANT: BASIOUX, LAURENT
##PAPLICANT: BASIOUX, LAURENT
##PAPLICANT: BASIOUX, LAURENT
##PAPLICANTON: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
##PAPLICANTON NUMBER: US 60/126,903
##PRIOR PILING DATE: 1999-03-30
##PRIOR FILING DATE: 1999-04-30
##PRIOR FILING DATE: 1999-04-30
##PRIOR FILING DATE: 1999-04-30
##PRIOR FILING DATE: 1999-07-29
##PRIOR FILING DATE: 1999-10-28
##PRIOR FILING DATE: 1999-10-12
##PRIOR FILING DATE: 1999-10-13
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                                                                                                                                                               Query Match
42.7%; Score 25.6; DB 4; Length 396;
Best Local Similarity 63.8%; Pred. No. 2.6;
Matches 37; Conservative 0; Mismatches 21; Indels
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OTHER INFORMATION: exon Bbis g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C 935018 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09539333D Patent No. 6476208
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-156
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
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NAME/KEY: misc feature
LOCATION: 31..1107
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LOCATION: 14877..14920
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LOCATION: 1108
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Page

LOCATION: 231272..231412 OTHER INFORMATION: exon Obis complement 934872 gene FEATURE: NAME/KEY: exon LOCATION: 292653..292841 'EATURE: !AME/KEY: exon .OCATION: 215819..215975 JTHER INFORMATION: exon Rbis complement 934872 gene FEATURE: NAME/KEY: exon LOCATION: 216661..216952 OTHER INFORMATION: exon Qbis complement g34872 gene NAME/KEY: misc feature JOCATION: 65854..67854 OTHER INFORMATION: 3'regulatory region g35018 gene TANENCEY: misc feature OCATION: 213818..215818 THER INFORMATION: 3'regulatory region g34872 gene WAME/KEY: exon LOCATION: 217027..217061 DTHER INFORMATION: exon Q1 complement 934872 gene PEATURE:
NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene |AME/KEY: exon |ACATION: 215819..215941 | JOHER INFORMATION: exon R complement 934872 gene WAME/KEY: exon COCATION: 216661..217061 DIHER INFORMATION: exon Q complement g34872 gene NAME/KEY: exon LOCATION: 229647..229742 OTHER INFORMATION: exon X complement g34872 gene FEATURE:
NAME/KEY: exon
LOCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene NAME/KEY: exon LOCATION: 29388..29502 OTHER INFORMATION: exon D 935018 gene NAWE/KEY: exon LOCATION: 29967..30282 OTHER INFORMATION: exon E g35018 gene MME/KEY: exon ACATION: 201188..201234 THER INFORMATION: exon S 935030 gene /KEY: exon IION: 215702..215746 R INFORMATION: exon U g35030 gene ME/KEY: exon OCATION: 216836..216915 'HER INFORMATION: exon V 935030 gene OCATION: 65505..65853 THER INFORMATION: exon G 935018 gene AME/KEY: exon OCATION: 214676..214793 THER INFORMATION: exon T 935030 gene IAME/KEY: exon JOCATION: 94124..94964 OTHER INFORMATION: exon g35017 IAME/KEY: exon

CATION:

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0; Gaps
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NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 240528..240596
JTHER INFORMATION: exon M1090 complement g34872 gene
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LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
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NAME/KEY: exon
LOCATION: 240528..240644
LOCATION: 240528..240644
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240824
OCHER INFORMATION: exon M862 complement g34872 gene
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NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
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JHER INFORMATION: exon Nbis complement g34872 gene
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NAME/KEX: misc_feature
NAME/KEX: misc_feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
FEATURE:
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LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
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LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
                                                                                      NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon 01 complement g34872 gene
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JOCATION: 239719..239807
THER INFORMATION: exon N2 complement g34872 gene
FRATURE:
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NAME/KEY: exon
LOCATION: 240528.241685
OTHER INFORMATION: exon M1 complement g34872 gene
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NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
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LOCATION: 239719..239853
DTHER INFORMATION: exon N complement g34872 gene
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42.7%; Score 25.6; D
Best Local Similarity 77.5%; Pred. No. 11;
Matches 31; Conservative 0; Mismatches
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MANE/KRY: allele
OCCHTON: 13.67

OTHER INFORMATION: 99-27941-150 : polymorphic base G or C
NAME/KRY: allele
OCCHTON: 21.672

OTHER INFORMATION: 99-27935-193 : polymorphic base G or C
NAME/KRY: allele
OCCHTON: 64485
OTHER INFORMATION: 99-27935-193 : polymorphic base G or C
NAME/KRY: allele
OCCHTON: 107231
OTHER INFORMATION: 99-21956-260 : polymorphic base A or G
OTHER INFORMATION: 99-24659-260 : polymorphic base A or G
OTHER INFORMATION: 99-24639-163 : polymorphic base A or G
OTHER INFORMATION: 99-24639-163 : polymorphic base A or G
OTHER INFORMATION: 99-24634-108 : polymorphic base A or G
OTHER INFORMATION: 99-24634-108 : polymorphic base A or G
OTHER INFORMATION: 99-24634-108 : polymorphic base A or G
OTHER INFORMATION: 99-5862-167 : polymorphic base A or G
OTHER INFORMATION: 99-5862-167 : polymorphic base A or G
OTHER INFORMATION: 99-5862-167 : polymorphic base A or G
OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
OTHER INFORMATION: 99-24658-410 : polymorphic base A or G
OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
OTHER INFORMATION: 99-24658-410 : polymorphic base A or G
OTHER INFORMATION: 99-24658-410 : polymorphic base A or G
OTHER INFORMATION: 99-30-313 : polymorphic base A or G
OTHER INFORMATION: 9-30-313 : polymorphic base A or G
OTHER INFORMATION: 8-300-221 : polymorphic base A or G
OTHER INFORMATION: 8-309-313 : polymorphic base A or G
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OTHER INFORMATION: 8-309-313 : polymorphic base A or G
OTHER INFORMATION: 8-309-313 : polymorphic base A or G
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OTHER INFORMATION: 8-309-313 : polymorphic base
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LOCATION: 205329
OTHER INFORMATION: 8-295-125 : polymorphic base C or T
                                                             NAME/KEY: exon
LOCATION: 246273..247802
OTHER INFORMATION: exon Z
NAME/KEY: misc_feature
LOCATION: 247803..249803
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 244353..244561
OTHER INFORMATION: exon Y
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cohen, Daniel
APPLICANT: Chamakov, Ilya
APPLICANT: Basioux, Laurent
ITLE OF INVENTION: SCITZOPHRENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS
ITLE REFERENCE: 53.USJS.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
CURRENT PILING DATE: 2000-03-03
PRIOR PILING DATE: 109/539,333
PRIOR PILING DATE: 109/510-03
PRIOR PLICATION NUMBER: 09/416,384
PRIOR PPLICATION NUMBER: 09/416,384
PRIOR PLICATION NUMBER: 60/168,088
PRIOR PLICATION NUMBER: 60/168,088
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                                                                                                  137819 GAATTTATGCTTTTCAGTGCTGGAAGCATTATAGAGGTTG 137858
                                14 GAATTTTTGCTTTTCATGCTGGAACTATGTTAAAGTTTG 53
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LOCATION: 199122..201122
OTHER INFORMATION: 5 regulatory region
NAME/KEY: exon
LOCATION: 201123..201234
OTHER INFORMATION: exon S
NAME/KEY: exon
LOCATION: 201123..201560
OTHER INFORMATION: exon S2
                                                                                                                                                                                                                                                                  Sequence 1, Application US/09679409
Patent No. 6555316
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
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DTHER INFORMATION: exon V2

NAME/KEY: exon
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OCATION: 217671..217764
THER INFORMATION: exon V1
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THER INFORMATION: exon W2
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INFORMATION: exon V4
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DIHER INFORMATION: exon U
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LOCATION: 240440..240673
OTHER INFORMATION: exon W
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OTHER INFORMATION: exon X
NAME/KEY: exon
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INFORMATION: exon V
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LOCATION: 227655..227736
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OCATION: 238715..238919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: exon
ACATION: 214676..214793
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                       RESULT 8
US-09-679-409-1
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Query Match
Best Local Similarity
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FILE REFERENCE: 785
   US-09-328-352-3500/c
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: polymorphic base A or G
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                                                : polymorphic base A
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Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 211132
OTHER INFORMATION: 8-282-92:
NAME/KEY: allele
LOCATION: 211247
OTHER INFORMATION: 8-281-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                            CCATION: 210361

THER INFORMATION: 8-283-278

NAME/STS: allele

CCCATION: 210463

THER INFORMATION: 8-283-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: 210583
TYHER INFORMATION: 8-283-56
NAME/KEY: allele
OCCATION: 210879
THER INFORMATION: 8-282-345
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LOCATION: 211315
OTHER INFORMATION: 8-281-299
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LOCATION: 211366
OTHER INFORMATION: 8-281-248
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LOCATION: 212821
OCHER INFORMATION: 8-278-289
NAME/KEY: allele
   OTHER INFORMATION: 8-293-130
                                                                                                                                                                AME/KEY: allele
CCATION: 208960
WHER INFORMATION: 8-287-249
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                    NAME/KEY: allele
LOCATION: 206545
27HER INFORMATION: 8-292-198
NAME/KEY: allele
                                                                                                 8-251-322
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                                                                                                                                                                                                                                                 INFORMATION: 8-287-86
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OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 210583
                                                                                                               NAME/KEY: allele
LOCATION: 208285
OTHER INFORMATION:
                                                                               LOCATION: 207313
DIHER INFORMATION:
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JOCATION: 211050
JTHER INFORMATION:
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OCATION: 209123
                                                                                                                                                                                                                                                                                                               AME/KEY: allele
OCATION: 210361
                                                                                                                                                                                                                                                                                                                                                                                                             KEY: allele
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LOCATION: 212520
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137819 GAATTTATGCTTTTCAGTGCTGGAAGCATTATAGAGGTTG 137858

RESULT 9

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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NAMENINI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3500
LENGTH: 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 ACCACAGITICGIGAAGCITIGGCITIAGACIGCIGCAGCIGITCIAAAGITIGAIAAGC
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Pred. No. 14;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-345-468-15/c
is Sequence 15, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Ulleval, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Valuchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF;
; FILE REFERENCE: 7853-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Busfield, S.
Villeval, J.
Jandrot-Perrus, M.
Vainchenker, W.
VENTION: GLYCOPROTEIN VI AND USES THEREOF
NCE: 7853-147
                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                           Score 23.8; DB 4;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
Sequence 3500, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-414-453A-15/c
; Sequence 15, Application US/09414453A
Patent No. 6383779
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3500
                                                                                                                                                                                                                                                                                                                                                                           ch 39.7%;
11 Similarity 62.7%;
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-345-468-15
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Job time : 35.75 secs
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                                                                                                                  Length 939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                     17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Willeval, S.
APPLICANT: Villeval, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Jandrot-Perrus, M.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/414,453A
CURRENT FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/345,468
FRIOR APPLICATION NUMBER: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Unleval, S.
APPLICANT: Villeval, J.
APPLICANT: Villeval, J.
APPLICANT: Jandrot-Perrus, M.
APPLICANT: Jandrot-Perrus, M.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REPERENCE: 7853-147;
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTESQ for Windows Version 3.0
                                                                                                                  DB 4;
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Pred. No. 14;
0; Mismatches
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                                                                                                                                                     0; Mismatches
                                                                                                                  Score 23.8;
Pred. No. 14
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Patent No. 6383779
                                                                                                                                                                                                                                                                                   RESULT 12
US-09-345-468-14/c
; Sequence 14, Application US/09345468
; Patent No. 6245527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.7%;
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il Similarity 66.7%;
34; Conservative
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Best Local Similarity 66.7
Matches 34; Conservative
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Best Local Similarity 66.7
Matches 34; Conservative
                                                        ; ORGANISM: Mus musculus US-09-414-453A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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                                                                                                              Query Match
Best Local Similarity
Matches 34; Conserv
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US-09-414-453A-14/c
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LENGTH: 1163
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SEQ ID NO 15
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                                            TYPE: DNA
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2 CAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTT 52

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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: GARY EN DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 901
LENGTH: 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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325 CGATACCGTCCAGCATTACTTCTTTCCATGGTTGGAATGAAGAAAGTCT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.7%; Score 23.8; DB 4; Length 5708; 66.7%; Pred. No. 20; ive 0; Mismatches 17; Indels 0
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                                                                                                                                                                                                                                   APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GRNES EXPRESSED IN ALZHEIMER'S DISEASE FILE REFERENCE: PA-0024 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6682888 331744.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.4; DB pred. No. 18; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SEQ TRARE: PERL Program
SEQ ID NO 21
LENGTH: 5708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June 3, 2004, 00:56:20
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Patent No. 6673910
                                                                                                                                                       Sequence 21, Application US/09566921 Patent No. 6682888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.2%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 34; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-540-236-901
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                                                                                                                                    US-09-566-921-21
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model Run on:

2, 2004, 23:14:04; Search time 141 Seconds June

(without alignments)
1941.275 Million cell updates/sec

US-10-069-056-7 60 Perfect score:

1 acaagagcctgcagaatttt......atgttaaagtttgccatgct 60 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2995936 seqs, 2280998010 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications NA:*

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13: /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US60_NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. c 1 c 2	Score 27.2 27.2	Query Match 45.3	Query Match Length DB	DB 13 16	US-10-027-632-46349 US-10-027-632-46349	Description Sequence 46349, A Sequence 46349, A	46349, A
	26.6	44.3	438	13	US-10-027-632-80814	Sequence 8	80814, A
	26.6	44.3	438	13	US-10-027-632-80815	Sequence 6	80815, A
	26.6	44.3	438	16	US-10-027-632-80814	Sequence 8	80814, A
	26.6	44.3	438	16	US-10-027-632-80815	Sequence 80815,	30815, A
_	25.6	42.7	396	6	US-09-825-294-156	Sequence 15	6, App
_	25.6	42.7	396	σ	US-09-970-966-156	Sequence 156, App	i6, App
_	25.6	42.7	396	15	US-10-212-677-156	Sequence 1	.56, App
_	25.6	42.7	396	16	US-10-361-811-156	Sequence 1	.56, Apr
	25.6	42.7	396	16	US-10-369-186-156	Sequence 156, App	56, Apr
	25.6	42.7	113306	16	US-10-292-798-1007	Sequence 1	.007, AK
_	25.6	42.7	319608	16	US-10-147-603-1	GENERAL INFORMATI	JFORMAT]
	25.4	42.3	1392	12	US-10-363-426-1	Sequence 1, Appli	., Appli

Sequence 3339, Ap	Sequence 127, App	Sequence 3, Appli				Sequence 250, App	Sequence 3838, Ap	Sequence 3838, Ap	Sequence 976, App	Sequence 19214, A	Sequence 15, Appl		Seguence 45, Appl	7,	Sequence 15, Appl	4	45	Sequence 47, Appl	14,	v	31,	1216	Sequence 6431, Ap	Sequence 283, App	ñ		63	Sequence 184, App	2029	Sequence 9356, Ap
US-10-029-386-3339	US-10-101-510-127	US-10-270-144-3	US-10-027-632-119183	US-10-027-632-119183	US-10-087-192-1567	US-10-087-192-250	US-09-938-842A-3838	US-09-938-842A-3838	US-10-087-192-976	US-09-814-353-19214	US-09-832-312-15	US-09-832-312-43	US-09-832-312-45	US-09-832-312-47	US-09-829-495-15	US-09-829-495-43	US-09-829-495-45	US-09-829-495-47	US-09-832-312-14	US-09-829-495-14	US-10-157-669-31	US-10-108-260A-1216	US-10-032-585-6431	US-10-341-961A-283	US-09-900-425A-1	US-10-079-185-1	US-10-369-022-63	US-10-310-154-184	US-10-087-192-2029	US-09-918-995-9356
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41.7	41.3	41.0	40.7	40.7	40.7	40.7	40.0	40.0	40.0	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.3
25	24.8	24.6	24.4	24.4	24.4	24.4	24	24	24	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.6
15	16	17	18	19	20	21	22	23	24	25	56	21	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Sequence 46349, Application US/10027632
Publication No. US20020198371A1
Fubblication No. US20020198371A1
GENERAL INFORMATION:
APPLICAMY: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-12
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 2000-02-24
FRIOR PELING DATE: 1139-11-23
FRIOR FILING DATE: 1139-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-3
FRIOR FR US-10-027-632-46349/c

ö Gaps ö Length 501; Indels Query Match 45.3%; Score 27.2; DB 13; Best Local Similarity 80.0%; Pred. No. 5.8; Matches 32; Conservative 0; Mismatches 8;

; TYPE: DNA ; ORGANISM: Human US-10-027-632-46349

Gaps

Indels

Length 438;

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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-07-120

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PELING DATE: 2000-02-24

PRIOR PELING DATE: 2000-02-24

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-09-18

PRIOR PELING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: PASLEEQ for Windows Version 4.0

SEG ID NOS 80815

LENGTH: 438
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERBNCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-300
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PAPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                              44.3%; Score 26.6; DB 13; 68.6%; Pred. No. 9.3;
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68.6%; Pred. No. 9.3;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 80814
LENGTH: 438
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Sequence 80814, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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nes 35; Conserv
                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-80814
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US-10-027-632-80815
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Best Local S:
Matches 35,
                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                Sequence 46349, Application US/10027632

Sequence 46349, Application US/10027632

Publication No. US2030204075A9

GRNERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: NUMBER: US 60/1218,006

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-08-09

PRIOR PILING DATE: 1999-08-08

PRIOR PILING DATE: 1999-08-09

PRIOR PILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REPERBUCE: 108827.129
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/165,218
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-09-28
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                                                                           482 irrargarrrcccrggcrggracrargrcaragcr
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APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 80.0
Matches 32; Conservative
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US-10-027-632-46349
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GENERAL INFORMATION:
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/199,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26.6; DB
Pred. No. 9.3;
1; Mismatches
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44.3%; Score 26.6; DE
Best Local Similarity 68.6%; Pred. No. 9.3;
Matches 35; Conservative 1; Mismatches
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 80815, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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Best Local Similarity 68.6%;
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
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US-10-027-632-80815
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                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 80814
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308 ANGACAATCAAAACATTTGCTTTNAGTGGCAGGAACACTGGTACATTTTTACTTGCT 365
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US-09-970-966-156
Sequence 156, Application US/09970966
Patent No. US20020173638A1
FRENERAL INFORMATION:
APPLICANT: NOISEM, David Alan
APPLICANT: Fling, Steven P.
APPLICANT: Ring, Steven P.
APPLICANT: AND USAGNOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 396;
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Pling, Steven P.
APPLICANT: Pling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER PILE REFERENCE: 210121.484C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25.6; DB 9;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.7%; Score 25.6; D
Best Local Similarity 63.8%; Pred. No. 21;
Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 156
LENGTH: 396
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/825,294 CURRENT FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 156, Application US/10212677; Publication No. US20030129192A1; GENERAL INFORMATION: APPLICANT: Chenault, Ruth A. APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 11, 30, 32, 37, 309, 332
OTHER INFORMATION: n = A,T,C or G
US-09-970-966-156
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(396)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapien
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NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 156
LENGTH: 396
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CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-246789
PRIOR FILING DATE: 2001-6-18
                                                                                                                                                               | FEATURE:
| NAME/KEY: misc feature
| LOCATION: 11, 30, 32, 37, 309, 332
| COTHER INFORMATION: n = A,T,C or G
| US-10-369-186-156
2003-02-14
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Best Local Similarity 77.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY: CDS
, LOCATION: (112891)..(113106)
US-10-292-798-1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
(11526)..(12452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS (37954)..(38097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (98732)..(98784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1) .. (113306)
                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS (201)..(207)
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-292-798-1007/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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| Publication No. US20030206918A1
| GENERAL INFORMATION:
| APPLICANT: Faling, Steven P.
| APPLICANT: Fling, Steven P.
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C8
| CURRENT FAPLICATION NUMBER: US/10/361,811
| CURRENT FILING DATE: 2003-02-05
| NUMBER OF SEQ ID NOS: 293
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 156
| LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 396;
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               APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF CVARIAN CANCER
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 156, Application US/10369186
Publication No. US20030232056A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.484C9
CURRENT APPLICATION NUMBER: US/10/369,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25.6; DB 16; Length 3
Pred. No. 21;
0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.7%; Score 25.6; 63.8%; Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: 11, 30, 32, 37, 309, 332
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: 11, 30, 32, 37, 309, 332
; OTHER INFORMATION: n = A,T,C or G
US-10-361-811-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Conservative
Fanger, Gary R.
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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US-10-361-811-156
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US-10-369-186-156
                                                                                                                                                                                                                                      SEQ ID NO 156
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Sequence 1007, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ASINATMA, YUTAKA
APPLICANT: ASINATMA, TUTAKA
APPLICANT: ASINATMA, TUTAKA
ITITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
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                                                                      0; Gaps
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                                                                                                                            3 AAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
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      Length 396;
Query Match 42.7%; Score 25.6; DB 16; Length Best Local Similarity 63.8%; Pred. No. 21; Matches 37; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.4e+02;
0; Mismatches 9;
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FEATURE:
NAME/KEY: allele
LOCATION: 149113
OTHER INFORMATION: polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 151637
OTHER INFORMATION: polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 151748
OTHER INFORMATION: deletion G
FEATURE:
FEATURE:
FEATURE:
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LOCATION: 151769
OTHER INFORMATION: polymorphic base A or G
FERTURE:
NAME/KEY: allele
LOCATION: 151847
OTHER INFORMATION: polymorphic base C or T
FEATURE:
                                                                                                                                                                                                                                                                                                                                                   MANEACKES: allele
LOCATION: 129789
LOCATION: 129789
FORMER: INFORMATION: polymorphic base C or G
FORMER: ALlele
LOCATION: 130777
OTHER INFORMATION: polymorphic base A or G
FEATURE:
NAMEACKES: allele
LOCATION: 136942...136944
OTHER INFORMATION: deletion ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANEACKEY: allele
LOCATION: 143839
OTHER INFORMATION: polymorphic base A or T
PEATURE:
NAME/KEY: allele
LOCATION: 146668
LOCATION: 146668
LOCATION: 126668
LOCATION: 126668
LOCATION: 147281
OTHER INFORMATION: polymorphic base C or T
FEATURE:
FEATURE:
FEATURE:
FEATURE:
NAME/KEY: allele
LOCATION: 120573
OTHER INFORMATION: polymorphic base A or
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 147505
OTHER HIFORMATION: polymorphic base G
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 148372
JTHER INFORMATION: polymorphic base A
                                                                                                                                                                               polymorphic base A
                                                                                                                                                                                                           FEATURE:
NAME/KEY: allele
LOCATION: 126105
OTHER INFORMATION: polymorphic base
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 148183
UTHER INFORMATION: deletion
                                                                                                                         NAME/KEY: allele
LOCATION: 121527
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 149012
OTHER INFORMATION:
                                                                                                APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: Chumanfeld, Marta
APPLICANT: Chumanfeld, Marta
APPLICANT: Chumanfeld, Marta
APPLICANT: Chumanfeld, Marta
APPLICANT: Budgueleret, Lydie
APPLICANT: Basioux, Laurent
APPLICANT: Chumanger: 05/10/147,603
CURRENT APPLICATION NUMBER: 05/10/130
PRIOR APPLICANTON NUMBER: US 60/126,903
PRIOR PLING DATE: 1999-00-30
PRIOR PLING DATE: 1999-00-30
PRIOR PLING DATE: 1999-00-40
PRIOR PLING DATE: 1999-00-40
PRIOR PPLING DATE: 1999-00-40
PRIOR PPLING DATE: 1999-00-40
PRIOR PPLING DATE: 1999-00-40
PRIOR APPLICANTON NUMBER: US 60/146,453
PRIOR PPLING DATE: 1999-07-29
PRIOR PPLING DATE: 1999-07-29
PRIOR PLING DATE: 1999-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: allele
LOCATION: 112468
OTHER INFORMATION: polymorphic base G or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME:
NAME:
SACTION: 119526
OTHER INFORMATION: polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
ADME/KEY: allele
ACCATION: 111978
JTHER INFORMATION: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION: 118972
WHER INFORMATION: polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: 119321
OTHER INFORMATION: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 110222
OTHER INFORMATION: polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 119316
JTHER INFORMATION: polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VALUE:
NAME/KEY: allele
LOCATION: 119160..119161
OTHER INFORMATION: deletion TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
COCATION: 117324..117327
JTHER INFORMATION: deletion ACTT
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Sequence 3339, Application US/10029386
Bublication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT PAPLICATION NUMBER: US/10/029,386
CURRENT FILING DAVE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AAGGACAGGAAGAATATTTTTTTTCATGTTTGGAGCTATGCCAAGGTGTTATATTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 cerceagaagrerrecrrecerreceregaagaareraaagaacrecere 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATG 58
                                                                                                                                                                                                                                                                                                                                                                   Score 25.4; DB 12; Length 1392;
Pred. No. 38;
0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAP TO CHR17.1

EXPRESSED IN LUNG, SIGNAL = 1.1

EXPRESSED IN BRAIN, SIGNAL = 0.62

EXPRESSED IN BONE MARROW, SIGNAL = 0.57

SMISSPROT HIT: Q9PDE1, EVALUE 3.40e-02

EST_HUMAN HIT: BE082725.1, EVALUE 8.00e-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.7%; Score 25; DB 15; Length 564;
64.9%; Pred. No. 40;
.ive 0; Mismatches 20; Indels
APPLICANT: Dohrmann, Cord
TITLE OF INVENTION: Novel Functions For DP214
                                                        CURRENT APPLICATION NUMBER: US/10/363,426
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: PCT/EP01/10076
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: DE 100 43 227.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
LENGTH: 1392
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: chicken embryos
US-10-363-426-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA

OGGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRES;
OTHER INFORMATION: EXPRES;
OTHER INFORMATION: EXPRES;
OTHER INFORMATION: SWISS!
OTHER INFORMATION: WINSS!
OTHER INFORMATION: WISS!
US-10-029-386-3339
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US-10-029-386-3339
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Pred. No. 2e+02;
0; Mismatches 9;
                  OCATION: 152691
THER INFORMATION: polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: polymorphic base A or
                                                                               NAME/KEY: allele
LOCATION: 152766
OTHER INFORMATION: polymorphic base A
                                                                                                                                                                     NAME/KEY: allele
LOCATION: 153046
JTHER INFORMATION: polymorphic base
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OTHER INFORMATION: polymorphic base
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OTHER INFORMATION: polymorphic base
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WHER INFORMATION: polymorphic base
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THER INFORMATION: polymorphic base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: allele
CCCATION: 156448
OTHER INFORMATION: polymorphic base
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Best Local Similarity 77.5%;
Matches 31; Conservative
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LOCATION: 155802
OTHER INFORMATION:
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LOCATION: 153123
THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: 153977
THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 154677
OTHER INFORMATION:
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INFORMATION:
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NAME/KEY: allele
LOCATION: 158172
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AME/KEY: allele
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LOCATION: 157897
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Search completed: June 3, 2004, 03:14:07 Job time : 143 secs

137819 GAATTTATGCTTTTCAGTGCTGGAAGCATTATAGAGGTTG 137858

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RESULT 14
US-10-363-426-1/c
US-10-363-426-1/c
; Sequence 1, Application US/10363426
; Publication No. US20040072773A1
; GENERAL INFORMATION:

14 GAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTG

53

26.8 44.7 736 28 BZ099915 26.6 44.3 604 28 CC163180 26.6 44.3 919 29 CG002247 26.4 44.0 529 13 BQ518948 26.4 44.0 561 28 BH167726 26.4 44.0 572 12 BM407497	11 26.4 44.0 577 13 BQ518947 12 26.4 44.0 871 29 CNS02P8M 13 26.2 43.7 846 13 BX722972 14 26.2 43.7 845 13 BX722972 15 26.2 43.7 853 13 BX718662 16 26.2 43.7 890 13 BX718661 17 26.2 43.7 890 13 BX718661 18 26.2 43.7 894 13 BX718661 26.2 43.7 391 29 CG334320 26.2 43.7 31.43 29 CG334320	010648666	25.6 42.7 327 28 AQ602351 25.6 42.7 410 14 CD188322 25.6 42.7 410 14 CD188324 25.6 42.7 432 14 CD188324 25.6 42.7 655 13 EXIOLB51 25.6 42.7 675 29 AG164724 25.4 42.3 325 28 AZ777859 25.4 42.3 325 28 CC166192 25.4 42.3 422 28 CC166192 25.4 42.3 425 28 CC166191 25.4 42.3 465 10 BB150479	RESULT 1 BX16321/c LOCUS LOCUS LOCUS DEFINITION Danio rerio genomic clone DKEY-145E6, genomic survey sequence. ACCESSION BX163231. RX163231 RX1632	TITLE Direct Submassion JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished COMMENT This sequence was generated from the T7 end of BAC 145E6. 145E6 is part of the Danlokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/. Location/Qualifiers 1.806 /organism="Danio rerio" //mol_type="genomic DNA" //db_xref="taxon:7955"
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model		Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: 55026578 . Minimum DB seq length: 2000000000 Maximum DB seq length: 2000000000 POSE-processing: Minimum Match 0% Listing first 45 summaries	Database : EST:* 1: em estba:* 2: em_esthum:* 3: em estin:* 4: em_estin:* 5: em estor:* 6: em estro:* 7: em estro:* 9: gb_est:* 11: gb_htc:* 12: gb_est2:* 13: gb_est3:* 14: gb_est4:* 15: em est4:* 15: em estfin:*	16: em_estcom: 17: em_gss_hum:: 18: em_gss_hum:: 19: em_gss_pin:: 20: em_gss_fun:: 21: em_gss_fun:: 23: em_gss_pino:: 24: em_gss_pino:: 25: em_gss_pino:: 26: em_gss_pino:: 27: em_gss_pino:: 29: em_gss_pino::	Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. ** Result

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SOURCE
ORGANISM
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
                                                                       AUTHORS
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NF100H01PL1F1014 Phosphate starved leaf Medicago truncatula cDNA
clone NF100H01PL 5', mRNA sequence.
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 543)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                     223 ACAAGGGTATGCAGGACTGTTACCTTACTTAGCTGGAACTATTTTCAAGTT 173
                                                                                                                                                              1 ACAAGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTT 51
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                                                                                    ch 50.3%; Score 30.2; DB 29; Length 806; 1 Similarity 74.5%; Pred. No. 33; 38; Conservative 0; Mismatches 13; Indels 0
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/clone="DKEY-145E6"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 48.0%; Score 28.8; D Similarity 75.0%; Pred. No. 90; 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           CG351810.1 GI:34269076
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002
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Matches 36; Conserv
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Elbases 1 to 668)

Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suebiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:st.81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="last"
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/dev_stage="trifoliate"
/dev_stage="trifoliate"
/dev_stage="trifoliate"
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/note="Vector: Lambda Zap; At the trifoliate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
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ophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Pan troglodytes DNA, clone: PTB-071D03.F, genomic survey sequence.
AG076861
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                               Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2000)
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
1510 San Solb 17325
Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mjharrison@noble.org
Insert Length: 617 Std Brror: 0.00
Plate: 100 row: H column: 01
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:3880"
   Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="NF100H01PL"
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Pan troglodytes
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4 AGAGCCTGCAGAATTTTTGCTTTTCATGCTTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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KEYWORDS
SOURCE
ORGANISM
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CG002247/c
                                                                                                                                                                                                                                        RESULT 6
CC163180/c
                                                                                                                                                                                                                                                                                                DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH230-237F3.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-237F3, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szkadogigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter dong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 237 row: F column: 3
Seg primer: SP6
Class: BAC ends.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Female"
/cell_type="Brain"
/clone_lib="CHOR1-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shatsbartsbern,A., Gebregeorgis,B., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 EçoRI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          392 GACCCTGCAAAACTTTCTCCTTTGCCAGCTGGCACAATGTTAACCTTTGTCA 443
                                                                                                                                                                                                                                                                                                                                                                                                     5 GAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCA 56
                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                   /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                      46.7%; Score 28; DB 29; Length 668; 71.2%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other GSSS: CH230-237F3.TV
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
This Ju Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                  /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-071D03.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10116"
/clone="CH230-237F3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                             Location/Qualifiers
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                                   : pKS145
Sequencing: -21M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ099915.1 GI:23740799
                                                                              SacI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                              37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         norvegicus
                                                                                                                      1. .668
                                                       R.Site 1
R.Site 2
                                       Vector
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
              LIBRARY
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VERSION
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AUTHORS
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JOURNAL
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BZ099915
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Inter-Organ: immature ears; Sire, 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one mucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (:x/y reads in M13mpl9; .b/g reads in pUC19). The same ligation was transformed into DH5a.
                                                                                                                                                                                                                                                                                                                                                                                   604 bp DNA linear GSS 29-APR-2003
ii60g10,b2 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
cc163180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 604)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombe, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
CHORI-230 Rat (BN/SBNHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="WGS-ZmaysF (DH5a methyl filtered)"
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                                                                                                                   Length 736;
                                                                                                                                                                                                                                                                              491 CAGCAGATITITICCTITITGAGGAGAAGTACTITIGGTAAAGTITIC 536
                                                                                                                                                                                                                                54
                                                                                                                                                                       Indels
                                                                                                                                                                                                                             9 CTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
PI=1: 516 367 8884
Pax: 516 367 8874
                                                                                                             Score 26.8; DB 28;
Pred. No. 3.7e+02;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.3%; Score 26.6; DB 28;
66.7%; Pred. No. 4.3e+02;
iive 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604.
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/clone="ii60g10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: shotgun
High quality sequence stop: 6
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mccombie@cshl.org
Plate: ii60 row: g colur
Seg primer: -21M13UnivFwd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="DH5a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC163180.1 GI:30190472 GSS.
                                                                                                             Query Match
Best Local Similarity 73.9%;
Matches 34; Conservative
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Gaps

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Indels

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Institute. Orders can be made through URL:
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Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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BH167726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST626363 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMJNO6 3' end, mRNA sequence.
CG002247
919 bp DNA linear GSS 19-AUG-2003
ZUAAMG3TV ZM 3.0_4.0 KB Zea mays genomic clone ZMMBPa0007L05,
genomic survey sequence.
CG002247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/clone="xwMBPa0007L05"
/clone llb="xm_3.04.0 kB"
/note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (Dases 1 to 529)

Buell, C.M., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of a set of potato cDNA clones for microarray analyses upublished (2002)
Other ESTSE: EST626362
Contact: Robin Buell
The Institute for Genomic Research
The Institute for Genomic Research
Email: potato-array@rigr.org
This clone can be obtained from the University of Arizona Genomics
                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD Calde, Panicoideae, Andropogoneae, Zea.

1 (Dases 1 to 919)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Click, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for maize Genomics
Unpublished (2002)
Other GSSS: ZUAMGITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 751 AGATICTACIGIGIATITITATITACATGITIGGCAATGITAATITITIGCIATACT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AGAGCCTGCAGAATTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26.6; DB 29;
Pred. No. 4.2e+02;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                  Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ518948.1 GI:21377817
                                                                                 CG002247.1 GI:33871666
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                                                                                                                                              Zea mays
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BQ518948/c
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AUTHORS
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JOURNAL
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                                                              ACCESSION
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561 bp DNA linear GSS 01-OCT-2001 VV SBa0001E02f Grape Vitis vinifera genomic clone VV_SBa0001E02f, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 561)
Towkins, J. P., Peterson, D.G., Main, D., Yang, T.J., Ablett, E.F.,
Towkins, J. P., Peterson, D.G., Maters, D. and Wing, R.A.
Development of Genomic Resources for Grape (Vitis vinifera L.): BAC
library construction, preliminary STC analysis, and Identification
of Clones Associated With Flavonoid and Stilbene Biosynthesis
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                   microarray analyses mixed potato tissues"
//note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
/Noi; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
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/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
                                                                                                                                                                                                                                                                                                                          'clone_lib="Generation of a set of potato cDNA clones for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%; Score 26.4; DB 13; Length 529; llarity 75.0%; Pred. No. 5e+02; Conservative 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GATTTCTCCATTTCCAGGCTCGAACTATATTAGTGTTTGCCAT 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Clemson University
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                             /mol_type="mRNA"
/cultivar="Kennebec or Binjte"
                                                                                      l. .529
/organism="Solanum tuberosum"
                                                                                                                                                                                                     /db xref="taxon:4113"
/clone="STMJN06"
/tissue_type="mixed tissues"
/lab_host="SOLR"
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/clone="VV_SBa0001E02f"
/tissue_type="Young leaves"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Vitis vinifera"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 419.
Location/Qualifiers
http://genome.arizona.edu/orders/
Seg primer: T7.
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/strain="Syrah"
                                        r: 1/.
.ocation/Qualifiers
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Query Match Best Local (

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Matches

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; sateritds; laminds; Solanales; Solanaceae; Solanum.

1 (Dases 1 to 57)

2 (Dases 1 to 57)

3 Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Karamycheva, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Generation of a set of potato cDNA clones for microarray analyses

1 Unpublished (2002)

Other ESTS: ESTS6283

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS02F8M 871 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 132A17 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
//note="Vector: pBluescript SK(-); Site_l: EcoRI; Site_2: Xhoi; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, eyes, tubers, or roots."
EST626362 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMJN06
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish, Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%; Score 26.4; DB 13; Length 577; 75.0%; Pred. No. 5e+02; ive 0; Mismatches 11; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Binjte"
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clone="STMJN06"
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AL194719.1 GI:7832825
GSS; genome survey sequence.
Tetraodon nigroviridis
                                                                                                                                                                     Solanum tuberosum (potato)
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                                                                                  BQ518947
BQ518947.1 GI:21377816
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                                                   mRNA sequence.
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DEFINITION
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CNS02F8M
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site_2:
XhoI; supplier: Cornell University, Tanksley lab;
Sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                         http://www.genome.clemson.edu/projects/stc/grape/VV_SBa To
order clones from this library see
http://www.genome.clemson.edu/orders"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM407497 572 bp mRNA linear EST 10-MAR-2003 EST581824 potato roots Solanum tuberosum cDNA clone CPR031114 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                         177 ACACGACCTTGAGGAATTTGTGATTCTATTAGCAAGAACTGTGTTCAGTAACTTTTGCT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Aken, S.,
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                            1 ACAAGAGCCTGCAGAATTTTTTTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT
                                                                                                                                                                                                                            Gaps
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van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Ake
Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.
Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Uppublished (2001)
Contact: Robin Buell
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Pred. No. 5e+02;
0; Mismatches 11; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                Score 26.4; DB 28; Length
Pred. No..5e+02;
0; Mismatches 21; Indels
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9712 Medical Center Dr, Rockville, MD 20850,

    .572
    /organism="Solanum tuberosum"

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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO31114"
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  analysis see
                                                                                                                                                                  44.0%;
65.0%;
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1 Similarity 75.0%;
33; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end, mRNA sequence.
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Best Local Similarity
Matches 33; Conserv
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EST

KEYWORDS SOURCE

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REFERENCE AUTHORS

TITLE JOURNAL

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DEFINITION

RESULT 10 BM407497 ACCESSION VERSION

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Gaps

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Estimate of human gene number provided by genome-wide analysis

TITLE

EST 07-MAR-2003

linear

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BQ518947

RESULT 11 BQ518947 LOCUS

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/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TNeu112i05"
          Sequencing primer: SP6.
Location/Qualifiers
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BX722972.1 GI:38395713
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67.38;
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                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL798699 AGC-neurula Silurana tropicalis cDNA clone TNeul12i05 5',
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This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dT primed from Sug of poly A+ RNA from neurula.

ECORI-NOII cut cDNA was then ligated into pCS107 with EcoRI at the

3. end and NoII at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site_2: NotI

Host: Escherichia coli DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tongo The Control of Section 1 (Dases 1 to 555)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Jun 25, 2002 this sequence version replaced gi:21584403.
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Genoscope sequence ID : C0AG132AA09LP1~end : T7"
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Pred. No. 4.9e+02;
2; Mismatches 8; Indels 0;
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/mol_type="genomic DNA"
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TROPICALIS_SEQUENCE_ID: TNeu112i05.plcSP6
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
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AUTHORS
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                                                                                                                              /dev_stage="neurula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Rogers, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.

CONSTRUCTED A Nigel Garrett.

CDNA was oligo dT primed from Sug of poly A+ RNA from tadpole embryos. ECGI-Not! cut cDNA was then ligated into pCS107 with ECGI at the 5' end and Not! at the 3' end.

Vector: pCS107; Site_1: ECGNI; Site_2: Not!

Host: Escherichia coli DH10B.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
43.7%; Score 26.2; DB 9; Length 555;
Best Local Similarity 67.3%; Pred. No. 5.7e+02;
Matches 37; Conservative 0; Mismatches 18; Indels (
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1 (bases 1 to 846)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. a
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone_lib="XGC-tadpole"
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Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Bmail: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 200
TROPICALIS_SEQUENCE ID: TTpA031m22.q1kT7
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/db_xref="taxon:8364"
organism="Silurana tropicalis"
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/clone lib="XGC-teadpole"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dr primed from EcoRI from tadpole embryos. EcoRI-votc cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Silurana.
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Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Sanger Institute
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18; Indels
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Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TTpA041j10.q1kT7
Sequencing primer: T7
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BX718662
BX718662.1 GI:38391403
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37; Conservative
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792 ACCCTGCACTATCGTTGCTGTTTATTTTTGGACCTATATGTAAGCGTACAATGCT 738 6 AGCCTGCAGAATTTTTTGCTTTTCATGGCTGGAACTATGTTAAAGTTTGCCATGCT 60 Š g

Query Match
43.7%; Score 26.2; DB 13; Length 853;
Best Local Similarity 67.3%; Pred. No. 5.6e+02;
Matches 37; Conservative 0; Mismatches 18; Indels 0

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3, 2004, 00:54:05 Search completed: June Job time : 1504.5 secs This Page Blank (uspto)

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Abb52755
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Hop laten Herbicida

Perfect score:

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Run

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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/note= "Wild type Thr substituted with Ala; This location corresponds to position 363 of the NS1 variant (T363A) shown in AAY72706"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parvovirus non-structure protein 1 (NS1) variant (T363A) peptide.
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ABJ20208
ABJ20207
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ABU05126
ABU05128
ABU05128
ABU05125
                    ABU12706
ABB52755
AAW17929
ABB93163
ABP69019
AAY82488
ABB12114
AAE26671
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(first entry)
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  WPI; 2001-212717/22.
N-PSDB; AAD02800.
Misc-difference
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31-MAY-2001
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118.967 Million cell updates/sec
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Adc96322 E
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                    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              1586107 segs, 282547505 residues
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Listing first 45 summaries
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NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                  Parvovirus non-structure protein 1 (NS1) variant (T394A)
                                                                                                                                                                                                                                                                                                                                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
     . 361 TRACRIFAFHGWNYVKVCHA 380
                                                              AAY72708 standard; protein; 672
                                                                                                                          (first entry)
                                                                                                                (revised)
                                                                                                                                                                                                                                                          Misc-difference 394
                                                                                                                                                                                                                                                                                                                                               13-AUG-1999;
                                                                                                                                                                                                                                                                                               EP1077260-A1
                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                       21-FEB-2001.
                                                                                                              06-AUG-2003
                                                                                                                                                                                                             Parvovirus
                                                                                                                                                                                                                         Synthetic.
                                                                                      AAY72708;
                                       RESULT 3
                                                    AAY72708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is parvovirus non-structure protein 1 (NSI) variant (7363A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                    NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 672;
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                                                                          Length 20;
                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                             Parvovirus non-structure protein 1 (NS1) variant (T363A).
                                                                         100.0%; Score 120; DB 4;
100.0%; Pred. No. 2.6e-11;
ive 0; Mismatches 0;
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100.0%; Score 120; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                            AAY72706 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 19-21; 41pp; English
                                                                                                                          1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                        99EP-00115161
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                                                                                                                                                                                                                                                                       (first entry)
                                                                                     Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rommelaere J;
                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-212717/22.
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                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                  Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1077260-A1
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31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                         Parvovirus.
Synthetic.
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                                                                          Query Match
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/note= "Wild type Thr substituted with Ala"

99EP-00115161.

Location/Qualifiers

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                                                                                                                                                                                                                                                                               (T394A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                             Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 116; DB 4;
Pred. No. 3.2e-09;
0; Mismatches 1;
                                                                                                                                                                                                              Claim 6; Page 25-27; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY72710 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 TRICRIFAFHGWNYVKVCHA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.7%;
95.0%;
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(first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
Nueesch J, Rommelaere J;
                                       WPI; 2001-212717/22.
N-PSDB; AAD02803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 672 AA;
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31-MAY-2001
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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA resplication and transcription activities, and the cytoloxicity activity. They evariants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                    Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.7%; Score 116; DB 4; Length 672; 95.0%; Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parvovirus non-structure protein 1 (NS1) variant (S283A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TRICRIFAFHGWNYVKVCHA 380
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRACRIFAFHGWNYVKVCHA 20
                                 99EP-00115161
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                                                                                                                                                Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 95.0
nes 19; Conservative
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                                                                                                                                                                                                      WPI; 2001-212717/22
                                                                                                                                                                                                                                    N-PSDB; AAD02797.
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N-PSDB; AAD02799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 672 AA;
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Misc-difference
                                 13-AUG-1999;
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31-MAY-2001
                                                                                                                                                Nueesch J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is parvovirus non-structure protein 1 (NSI) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
                                                         NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                          /note= "Wild type Thr substituted with Ala"
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Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
Parvovirus non-structure protein 1 (NS1) variant (T463A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Page 30-32; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumoural disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00115161.
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 95.0
es 19; Conservative
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N-PSDB; AAD02805.
                                                                                                                                                                                                                                       Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1999;
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                                                                                                                                                Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parvovirus
                                                                                                                                                                              Synthetic
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Query Match

Matches

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ABB71925;
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Matches
                                                      RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated on 24-OCT-2003 to standardise OS field)
                                        The present sequence is parvovirus non-structure protein 1 (NS1) variant (S283A). The invention relates to the variants of the parvovirus nonstructure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                      Sequence encoded by the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     ;
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                                                                                                                                                            96.7%; Score 116; DB 4; Length 672; 95.0%; Pred. No. 3.2e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

80.8%; Score 97; DB 1; Length 690;
Best Local Similarity 70.0%; Pred. No. 2.5e-06;
Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Protein envelope; immunogen; vaccine; antigen; epitope
  transcription activities, and cytotoxic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                          AAP40306 standard; protein; 690 AA
                       Claim 6; Page 14-16; 41pp; English
                                                                                                                                                                                                                        361 TRTCRIFAFHGWNYVKVCHA 380
                                                                                                                                                                                                           1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84WO-US000063.
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84US-00567968.
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                              Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1984-201354/32.
                                                                                                                                         Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 690 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1984;
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                                                                                                                                                                                                                                                                                                                                      24-OCT-2003
12-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1984
                                                                                                                                                                                                                                                                                                                                                                                   parvovirus
                                                                                                                                                                                                                                                                                                               AAP40306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fox GM;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 42567; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #23958.
                                                                                                                                                                                                             ABB71925 standard; protein; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG23967 standard; protein; 343 AA
                               362 TRTCKIFSMHNWNYIKVCHA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li PWD,
1 TRACRIFAFHGWNYVKVCHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 FHGWNIFKICN 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL16028
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                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymucleotides are also used and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disqual conditions in disquances of the invention. Note: The sequence blad and conditions and to order types of data and products dependent on DNA and and can order expressions of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the electronic format directly from WIPO at the will be printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 54326; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS88154
                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                     Homo sapiens
                                                                                                                                                                       11-OCT-2001
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Gaps
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                           40.0%; Score 48; DB 4; Length 343;
                                                     6; Indels
                                       Pred. No. 37;
2; Mismatches
                                                                                 2 RACRIFAFHGWNYVKVCH 19
                                          55.6%;
                                        Best Local Similarity 55.6
Matches 10; Conservative
Sequence 343 AA;
                             Query Match
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|| | |||| || :: | 152 RARAIVAFHGGNYRELYH 169

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Terpenoid biosynthesis related H64 strawberry protein #27.
              ADE82746 standard; protein; 554 AA
                                                 (first entry)
                                                 29-JAN-2004
                                ADE82746;
RESULT 10
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isoprenoid; bio-active compound synthesis; pesticide; dermatological;

cytostatic; immunosuppressive; virucide; flavour; fragrance; bio-control agent; food additive; food industry; pest control; degreasing solvent; plasticizer; dye carrier; dental caries; dental plaque; skin disorder; immunosuppressive; anti-leukaemia; anti-retroviral; monoterpene alcohol linalooi; sesquiterpene alcohol nerolidol; monoterpenoid; strawberry.

Fragaria x ananassa.

EP1231273-A1.

14-AUG-2002

12-FEB-2001; 2001EP-00200488.

12-FEB-2001; 2001EP-00200488, (PLAN-) PLANT RES INT BV Bouwmeester HJ Aharoni A, Verhoeven HA, Jongsma MA,

WPI; 2003-879727/82.

Novel recombinant nucleic acid encoding proteinaceous molecule, useful for producing flavor, fragrance and/or biocontrol agent which is useful as food additive in processed food industry and as antimicrobial agent.

Disclosure; Page; 52pp; English

recombinant isopremoin activities compound synthesis muciescal actu and its protestatic, immunosuppressive, and virucide. The novel recombinant isopremoid bio-active compound synthesis nucleic acid is useful for producing flavour. Fragrance, and/or a bio-control agent, by transforming or transfecting a suitable host with the recombinant isopremoid bio-active compound synthesis nucleic acid, expressing the recombinant isopremoid bio-active compound synthesis nucleic acid in the presence of a suitable substrate, and optionally isolating the formed product. The isopremoid bio-active compound synthesis nucleic acid in the presence of a suitable substrate, and optionally isolating the formed product. The bio-control agent is useful as an anti-microbial agent, as a food additive in the processed food industry to modify the taste of syrups, iso-control agent for oral medications and vitamins, and for providing a flavour/aroma in beverages, including alcoholic beverages. The bio-control agent is also useful for enhancing or reducing flavour, aroma in products, and for the industrial synthesis of nature identical flavour/aroma substances and/or artificial synthesis of nature identical flavour/aroma substances and/or artificial synthesis and insects and/or plants and microorganisms, for products, hair conditioners, cleaning communities, personal care products and health care products, as a composition of a composition of the interaction between plants and insects and/or plante substance and/or plante substance and/or plante substance and/or plante substance and/or plante is useful as a molecular marker or diagnostic tool. The protein fragments is useful as a molecular marker or diagnostic tool. The protein fragmostic tool. The protein are products or composition of a composition of the novel acid is useful for the production of an antagonist e.g. an antibody or the functional equivalent which is useful for inhibiting the synthesis of the bio-control agent. A composition, containing the bio-control agent, is a pharmaceutical or nutraceutical, useful for augmenting or enhancing the aroma and/or taste of food or non-food products, and/or protection of food or non-food products against fungal contamination and/or preterion of pests, for the protection of stored products and for the prevention or reatment. Pre composition is also useful for the prevention or treatment of disease. The bio-control agent is useful as a degreasing solvent, plasticizer and dye carrier. The composition is useful for replacing potentially carrinogenic synthetic food additives currently capable of isoprenoid bio-active compound synthesis when provided with a suitable substrate under appropriate reaction conditions. The novel recombinant isoprenoid bio-active compound synthesis nucleic acid and its fragments is useful as a molecular marker or diagnostic tool. The protein of the novel recombinant isoprenoid bio-active compound synthesis nucleic replacing potentially carcinogenic synthetic food additives currently used. The composition is also useful for treating dental caries, dental plaque and skin disorders, and for immunosuppressive, anti-leukaemia and The invention relates to a novel isolated or recombinant nucleic acid its functional fragment, encoding a proteinaceous molecule essentially

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The invention relates to a novel isolated or recombinant nucleic acid or its functional fragment, encoding a proteinaceous molecule essentially capable of isopremoid bio-active compound synthesis when provided with a suitable substrate under appropriate reaction conditions. The novel recombinant isopremoid bio-active compound synthesis nucleic acid and its protein have the following activites: pesticide, dermatological, cytostatic, immunosuppressive, and virucide. The novel recombinant isopremoid bio-active compound synthesis nucleic acid is useful for producing flavour, fragrance, and/or a bio-control agent, by transforming a transfecting a suitable host with the recombinant isopremoid bio-active compound synthesis acid, expressing the recombinant isopremoid bio-active compound synthesis nucleic acid in the presence of
                  compound synthesis nucleic acid or its protein is useful for the synthesis of monoterpen alochol linahool and sesquiterpene alochol nerolidol, and monoterpenoid. This sequence represents an H64 protein seed in the terpenoid biosynthesis method of the invention. NoTE: This sequence is not shown in the specification. It has been obtained from electronic data supplied with this specification from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant nucleic acid encoding proteinaceous molecule, useful for producing flavor, fragrance and/or biocontrol agent which is useful as food additive in processed food industry and as antimicrobial agent.
anti-retroviral treatment. The novel recombinant isoprenoid bio-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoprenoid, bio-active compound synthesis, pesticide, dermatological, cytostatic, immunosuppressive, virucide, flavour, fragrance, bio-control agent, food additive, food industry, pest control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degreasing solvent, plasticizer; dye carrier; dental caries; dental plaque; skin disorder; immunosuppressive; anti-leukaemia; anti-retroviral; monoterpene alcohol linalol; sesquiterpene alcohol nerolidol; monoterpene alcohol nerolidol nerol
                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 554;
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Pred. No. 59;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 SCKVYOKHGWNPLQSLKISWASLCNA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YVKVCHA 20
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26.9%;
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                        Sequence 554 AA;
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cc a suitable substrate, and optionally isolating the formed product. The bio-control agent is useful as an anti-microbial agent, as a food additive in the processed food industry to modify the taste of syrups, cc ice-creams, frozen desserts, yogurts, confectionery and like products, as a flow a flavouring agent for oral medications and vitamins, and for providing additional flavour/aroma in beverages, including alcoholic beverages. The cc aroma, fragrance or scent of plants, natural products, and/or synthetic or aroma, fragrance or scent of plants, natural products, and/or synthetic or archificial products, and/or synthetic or archificial products, and/or synthetic correction between plants and insects indentical flavour/aroma substances and/or artificial flavour/aroma commencing or artificial flavour/aroma in commencing or artificial gent is also useful as a pest control agent is also useful as a pest control agent or substances. The bio-control gent is also useful as a molecular marker or diagnostic tool. The protein products, personal care products and health care products, as a disinfectant additive and in the preparation of a composition. The novel crecombinant isopenoid bio-active compound synthesis nucleic acid or its fragments is useful for the products and health care products, and antibody or creaming a pharmaceutical or nutraceutical, useful for inhibiting the synthesis of the aroma and/or taste of food or non-food products, and/or protection of the aroma and/or taste of food or non-food products, and/or protection of treatment of disease. The bio-control agent is useful for the biological control of pests, for the protection of stored products and for the prevention or treatment of disease. The bio-control agent is useful for treatment of disease. The bio-control agent is useful for the biological control or creatment of disease. The bio-control agent is manipulation is also useful for control as a degreasing or creatment of disease. The bio-control agent is manipulated by a products and dye carrie ; plague and skin disorders, and for immunosuppressive, anti-leukaemia and anti-retroviral treatment. The novel recombinant isopremoid bio-active compound synthesis nucleic acid or its protein is useful for the synthesis of monoterpene alcohol linalool and sesquiterpene alcohol nerolidol, and monoterpenoid. This sequence represents an H64 protein used in the terpenoid blosynthesis method of the invention. NoTE: This sequence is not shown in the specification. It has been obtained from electronic data supplied with this specification from the European Patent Gaps Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. 8; Score 48; DB 7; Length 580; Pred. No. 62; 4; Indels 40.0%; Scor. 26.9%; Pred. No. 02, ... 7; Mismatches 383 SCKVYQKHGWNPLRSLKISWASLCNA 408 3 ACRIFAFHGWN-----YVKVCHA 20 Novel human diagnostic protein #23957. ABG23966 standard; protein; 598 AA 30-MAR-2001; 2001WO-US008631. (first entry) Sequence 580 AA; WO200175067-A2. Homo sapiens. 18-FEB-2002 11-OCT-2001. ABG23966; RESULT 12 ABG23966 셤 ਨੇ

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08-FEB-2002; 2002US-00072851
                                                                                                           WPI: 2003-029926/02
                                                                                                                           N-PSDB; ACA26867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU22127;
                                                                  Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. Ag600010-A8033377 represent novel human diagnostic amino acid sequences. Ag600010-A8033377 represent novel human diagnostic mino acid sequences. Ag600010-A8033377 represent novel human diagnostic datent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [Tep. wipo.int/pub/published_pct_sequences]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 48; DB 4; Length 598; 55.6%; Pred. No. 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #8524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                       Claim 20; SEQ ID NO 54325; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU22997 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 RARAIVAFHGGNYRELYH 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RACRIFAFHGWNYVKVCH 19
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                     Tang YT
31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                   Drmanac RT, Liu C,
                                                                                             WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                       (HYSE-) HYSEQ INC
                                                                                                           N-PSDB; AAS88153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 598 AA;
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                                                                                                                                                                               biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ABU22997
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  셤.
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The invention Fraces to an included acts compilately any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a propose expression is inhibited by the antisense concoding a polypeptide whose expression is inhibited by the antisense concoding a polypeptide whose expression is inhibited by the antisense continued by the antisense continued or its fragment whose expression is inhibited by the antisense continued to polypeptide; (3) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway confirmed for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity, (11) a culture comprising strains in which the extent compound that inhibits proliferation of an organism. The antisense mucleic acids are useful for proliferation of an organism. The antisense mucleic acids are useful for confidentifying proteins or screening for homologous nucleic acids required for for endidate modelic acids are useful for deach deach or the strains is present in a culture compound that inhibits for confidentifying the target of a compound that inhibits for collection of the strains in present in a culture compound that inhibits for collection of the strains is present in a culture acids are useful for dentifying proteins or screening for homologous nucleic acids required for proliferation to isolate condidate modelic acids required for actional and actional and actional actions are actived and actional actions and actional actions and actional actions are actived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                       Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 50921; 1766pp; English.
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172 RRILFHGWNWAQIEEMALPPCH 193
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                                                                                                                                                                                                       Malone C,
                                                                                                                                                                                                                                                            Carr GJ,
06-MAR-2002; 2002US-0362699P.
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Matches 8; Conservative
                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                       Zamudio C,
Trawick JD,
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2000US-0236368P. 2000US-0236369P. 2000US-0236370P. 2000US-0236802P.

000US-0237037P.

2000US-0237040P 2000US-0239937P 000US-0240960P 2000US-0241221P

2000US-0237039P

2000US-0241785P. 2000US-0241786P.

2000US-0241787P

2000US-0241808P. 2000US-0241809P.

000US-0241826P 000US-0244617P 000US-0246476P

2000US-0246523P

2000US-0234223P. 2000US-0234274P. 2000US-0234997P. 2000US-0234998P. 000US-0235834P 2000US-0236327P

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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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05-DEC-2000;
06-DEC-2000;
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 fungicide; cancer;
                  ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; carddrovascular disorder; cerebrovascular disorder; erebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
   cerebroprotective; nootropic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                      31.JAN-2000; 2000US-0179065P.
24-FEB-2000; 2000US-018665P.
22-MAR-2000; 2000US-0186456P.
22-MAR-2000; 2000US-0186456P.
16-MAR-2000; 2000US-0189874P.
11-MAR-2000; 2000US-0199076P.
18-APR-2000; 2000US-0199076P.
19-MAY-2000; 2000US-019813P.
19-MAY-2000; 2000US-02158P.
28-JUN-2000; 2000US-0215486P.
30-JUN-2000; 2000US-0216647P.
07-JUL-2000; 2000US-021668P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
26-JUL-2000; 2000US-02219689P.
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14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225758P.
18-AUG-2000; 2000US-0225758P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-022688P.
23-AUG-2000; 2000US-022688P.
23-AUG-2000; 2000US-022987P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229509P.
05-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
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14-AUG-2000; 2000US-0224519F.
14-AUG-2000; 2000US-0225213F.
14-AUG-2000; 2000US-022526F.
14-AUG-2000; 2000US-022526F.
14-AUG-2000; 2000US-025256F.
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2000US-0232400P
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14-AUG-2000;
                                                                                                                                                                   Homo sapiens
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2000US-0249215P. 2000US-0249216P. 2000US-0249217P.

:000US-0249218P

000US-0249265P 000US-0249299P

2000US-0251479

000US-0246611P

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000US-0246527P 2000US-0246532P 000US-0246609P 000US-0246610P 2000US-0249208P.

2000US-0249210P

2000US-0249211P. 2000US-0249212P.

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26-SEP-2000; 2000US-0235484P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU21852-AAU22466 represent the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynuclectides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition of adetermined by detecting the presence or a absence of a mutation in a cardiovascular system antigen polynuclectide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, the presentive disorders such as reoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as corneal infection, endocrine disorders such as glomentulonephritis and respiratory disorders such as satham and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, committed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cardiovascular system related polypeptide; cancer; proliferative disorder; foetal abnormality; developmental abnormality; hamematopidetic disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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39.2%; Score 47; DB 4; Length 54;
Best Local Similarity 53.3%; Pred. No. 8.8;
Matches 8; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                          2000US-0251990P.
                                                             2000US-0251868P
2000US-0251869P
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9 TSACQ--SYHSWNYV
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                                               07-MAR-2002; 2002US-00091504
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17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0259391P.
05-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0251988P.
06-DEC-2000; 2000US-0251988P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
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2000US-0249299P.
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The invention relates to human cardiovascular system related polypeptides and the polymucleotides encoding them. The polypeptides, polymucleotides and antibodies to the polypeptides are useful for diagnosing a and antibodies to the polypeptides are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular system tissues, proliferative disorders, feetal and developmental abnormalities, haematopoietic disorders, disease of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, cardiovascular disorders, angiogenic disorders, atherosclerosis, cardiovascular disorders, angiogenic disorders, and incorders, and incorders, and incorders, pregnancy-crelated disorders, machorine disorders and infections. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and polymucleotides are also useful for chromosome identification, radiation hybrid mapping or long-range capabilities, fat content or other mutritional components. This sequence represents a human cardiovascular system
                                                                                                                                                                                                                                                                                                                               New cardiovascular system related polynuclectides and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular tissues and cancer metastases.
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(HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                            Ruben SM,
                                                                                                                                                                                              WPI; 2003-743766/70.
N-PSDB; ADE45480.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 28, 2004, 12:52:43 ; Search time 10.5 Seconds (without alignments) 183.222 Million cell updates/sec Run on:

US-10-069-056-9 Title:

120 1 TRACRIFAFHGWNYVKVCHA 20 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADITES

	Description	noncapsid protein			ъ	ש	T					υ		hypothetical prote	putative tetrameri				probable ABC trans	coat protein - chr	conserved hypothet	C4-dicarboxylate t	choline monooxygen	LAT1 protein - hum	CDPdiacylglycerol-	protein T16A1.5 [i	p19 protein - beet	(apurinic o	protein -	p31 protein - beet
SUMMARIES	ID	UYPV1M	A44276	UYPVIM	UYPVV1	UYPVNA	UYPVPP	UYPV1F	UYPVCP	UYPVME	UYPVFP	T19406	D71842	C96638	G90104	T31646	T15249	T32479	T02491	JQ1250	A87602	C69771	T08550	JG0165	T11166	A88065	D44503	JC5235	'n	C44503
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	* Query Match Length	672	899	721	672	662	099	392	999	668	899	586	136	594	242	490	359	563	1443	315	389	421	426	507	521	123	135	278	282	282
	* Query Match	96.7	95.8	94.2	88.3	80.8	76.7	75.8	75.8	75.8	75.8	52.1	40.0	0	39.6	œ	38.3	38.3	37.9	37.5	37.5	36.7	36.7	36.7	36.2	35.8	35.8	5.	35.8	35.8
	Score	116	115	113	106	97	92	91	91	91	91	62.5	48	48	47.5	46.5	46	46	45.5	45	45	44	44	44	43.5	43	43	43	43	43
	Result No.		8	m	4	S	9	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	29

hypothetical prote	hypothetical prote	probable starch sy	pyruvate dehydroge	protein F2K11.20 [hypothetical prote	coat protein - pot	coat protein - pot	conserved hypothet	hypothetical prote	hydroxymandelonitr	hypothetical prote	cytochrome-c oxida	cytochrome-c oxida	cytochrome-c oxida	cytochrome-c oxida
S74431	T46355	S74473	AG0521	A96660	G85070	VCVYPV	A48549	AH3145	G72854	G71414	C98142	ODBY1	S17993	JU0148	S78640
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358	425	491	887	605	124	293	297	359	363	407	411	512	534	534	534
35.8	35.8	35.8	35.8	35.4	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0
43	43	43	43	42.5	42	42	42	42	42	42	42	42	42	42	42
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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RESULT 1
UYPV1M
noncapsid protein NS1 - minute virus of mice
c) Species: minute virus of mice, murine parvovirus
C) Species: minute virus of mice, murine parvovirus
C) Date: 14-Nov-1983 #sequence_revision 28-Aug-1985 #text_change 08-Apr-1994
C) Accession: A03696
C) Accession: A03696
A) Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A) Recession: A03696
A) MUD: 83143341; PMID: 6298737
A) Accession: A03696
A) MUD: 83143341; PMID: 6298737
A) Accession: A03696
C) Subperfamily: parvovirus noncapsid protein
C) Keywords: noncapsid protein

Gaps ö Query Match

96.7%; Score 116; DB 1; Length 672;
Best Local Similarity 95.0%; Pred. No. 1.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels

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1 TRACRIFAFHGWNYVKVCHA 20 ઠે

361 TRTCRIFAFHGWNYVKVCHA 380 g

RESULT 2

Cispecies: parvovirus LuIII
Cispecies: A4276
Ribiffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-345, 1993
A; Paccession: A44276
A; Accession: A44276
A; Accession: A44276
A; Accession: A44276
A; Accession: A44276
A; Status: translation not shown
A; Status: translation not shown
A; Residues: 1-668 < DIF>
A; Cross-references GB: M8188
A; Cross-references GB: M8188
C; Superfamily: parvovirus noncapsid protein
C; Keywords: noncapsid protein

95.8%; Score 115; DB 1; Length 668; 90.0%; Pred. No. 2.6e-10; tive 1; Mismatches 1; Indels 18; Conservative Query Match Best Local Similarity Matches 18; Conserv?

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Fibergeron, J.; Menezee, J.; Tijssen, P.
Virology 197, 86-98, 1993
A;File: Genomic organization and mapping of transcription and translation products of th
A;Reference number: A48472; MUID:94025614; PMID:8212598
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A;Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parvon, A;Reference number: A03697; MUID:85265017; PMID:2991581
A;Accession: A03697
A;Molecule type: DNA
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*Residues: 1-88,'R', 87-273,'R',275-375,'V',377-620,'NLH',623-624,'PTPPD',630,'AIR',634,
A;Cross-references: EMBL:M38367; NID:G332987; PIDN:AAA46920.1; PID:G332989
C;Superfamily: parvovirus noncapsid protein
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A; Molecule type: DNA
A;
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C;Species: porcine parvovirus
C;Species: a0-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jun-2000
C;Accession: A33302; B36217; A33743; A36217
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J;Gen. Virol. 70, 2541-2553, 1989
A;Fitle: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
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C;Species: feline panleukopenia virus, FPLV
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
                                    A;Molecule type: DNA
A;Residues: 1-662 <VAS>
A;Cross-references: EMBb:M38367; NID:9332987; PIDN:AAA46920.1; PID:9332989
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A;Experimental source: strain NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
C;Superfamily: parvovirus noncapsid protein
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65.0%; Pred. No. 1.1e-06;
tive 3; Mismatches 4; Indels
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70.0%; Pred. No. 1.8e-07;
tive 3; Mismatches 3; Indels
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                                                                                                                                                                      A; Experimental source: strain NADL-2
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Best Local Similarity 70.0°
Matches 14; Conservative
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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A; Accession: A36217
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C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: A03695
E;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybri
                                                                                                            noncapeid protein NSI - minute virus of mice (strain MVMi)
C;Species: minute virus of mice, murine parvovirus
C;Species: minute virus of mice, murine parvovirus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
C;Accession: A23008, A29510
R;Sahli, R.; McMaster, G.K.; Hirt, B.
Nucleic Acids Res. 13, 3617-3531, 1985
A;Title: DNA sequence comparison between two tissue-specific variants of the autonomous
A;Reference number: A23008; MUID:85242059; PMID:3855242
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NyAlternate names: nonstructural protein NS-1
C;Specises: porcine parvovirus
C;Specises: porcine parvovirus
C;Accession: A36217; A48472; A33743
C;Accession: A36217; A88472; A33743
C;Accession: A36217; A88472; A33743
A;Pitle: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Cross-references: EMBL:X02481
R;Astell, C.R.; Gardiner, B.M.; Tattersall, P.
J. Virol. 57, 656-669, 1986
A;Title: DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and A;Reference number: A29510; MUID:86115415; PMID:3502703
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A,Residues: 1-672 <RHO>
A,Cross-references: EMBL:X01457; NID:g60993; PIDN:CAA25689.1; PID:g60994; EMBL:J02198
C,Superfamily: parvovirus noncapsid protein
C,Keywords: noncapsid protein
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A;Molecule type: DNA
A,Rolecule type: DNA
A,Rossitues: 1.645,'I',647-721 <AST>
C,Superfamily: parvovirus noncapsid protein
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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85.0%; Pred. No. 6.9e-09;
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Best Local Similarity 85.0
Matches 17, Conservative
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A;Molecule type: DNA
A;Residues: 1-721 <SAH>
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UYPVNA
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Aritle: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvon A; Reference number: A36608; MUD:91073139; PMID:2174965
A; Accession: A36608
A; Molecule type: DNA
A; Residues: 1-668 < MAR>
A; Residues: 1-668 < MAR>
C; Superfamily: parvovirus noncapsid protein
C; Keywords: noncapsid protein
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C;Species: Helicobacter pylori
A;Variety: strain J99
E;Species: Helicobacter pylori
A;Variety: strain J99
C;Acte: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: D71842
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Jross, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; J Nature 397, J6-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathx A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-136 <ARN>
A;Cross-references: GB:AE001543; GB:AE001439; NID:g4155753; PIDN:AAD06732.1; PID:g4155754
A;Experimental source: strain J99
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A;Cross-references: EMBL:Z70034; PIDN:CAA93857.1; GSPDB:GN00020; CESP:C18E9.8
A;Experimental source: clone C18E9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C18E9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A;Introns: 158/3; 269/3; 354/3; 493/2; 538/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C18E9.8
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C;Superfamily: Helicobacter pylori hypothetical protein jhp1160
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                                                                                                                                                                                                                                                                                                 Score 91; DB 1; Length 668;
Pred. No. 1.7e-06;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Risims, M. submitted to the EMBL Data Library, March 1996 submitted to the EMBL Data Library, March 1996 A; Reference number: 219120 A; Accession: 119406 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 SRTCQIFRMHGWNWIKVCHA 381
                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRACRIFAFHGWNYVKVCHA 20
   Virol. 71, 2747-2753, 1990
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative ,
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Best Local Similarity
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A; Status: preliminary
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Cispecies: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
Ciscession: A38350
Ciscession: A38350
Aritle: Construction and nucleotide sequence analysis of an infectious DNA clone of the Arritle: Construction and nucleotide sequence analysis of an infectious DNA clone of the Arecession: A38350; MUD:91202123; PMID:2016597
Arccession: A38350; MUD:91202123; PMID:2016597
Arccession: A38350; MID:91202123; PMID:BAA00662.1; PID:g222436
Ciscestion: Ciscession: A38350; MID:g222435; PIDN:BAA00662.1; PID:g222436
Ciscestion: Ciscession: Astronomeropsid protein
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A36608
R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noncapsid protein NS1 - canine parvovirus (strain N)
C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29962
A, Residues: 1-392 < CAR>
A, Cross-references: EMBL:M10824; NID:g333474; PIDN:AAA47160.1; PID:g333475
C, Superfamily: parvovirus noncapsid protein
C; Keywords: noncapsid protein
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A,Molecule type: DNA
A,Residues: 1 -668 EMES-
A;Cross-references: EMBL:M19286; NID:g333438; PIDN:AAA67459.1; PID:g333439
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: A29962
R;Red, A.P.; Jones, B.V.; Miller, T.J.
Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine parvovirus.
A;Reference number: A29962; MUID:88062992; PMID:2824850
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                                                                                                                                                Query Match 75.8%; Score 91; DB 1; Length 392; Best Local Similarity 65.0%; Pred. No. 9.9e-07; Matches 13; Conservative 4; Mismatches 3; Indels
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Pred. No. 1.7e-06;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                 86 SRICQIFRMHGWNWIKVCHA 105
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Best Local Similarity 65.v.
Best Local 3; Conservative
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hypothetical protein Y57A10A.x - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CESP:Y57A10A.x
A;Introns: 89/2; 244/2; 423/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.x
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues: 1-490 <WIL>
A; Cross-references: BMBL:AL117195; PIDN:CAB55029.1; CESP:Y57A10A.x A; Experimental source: clone Y57A10A
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38.8%; Score 46.5; DB 2; Length 490;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 1; Indels
                                - Caenorhabditis elegans
                                                                                                                                                                                                                                              Rismye, R. submitted to the EMBL Data Library, September 1999 A; Reference number: 221048 A; Reference number: 24 A; Reference number: 25 A; Reference
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G190104

putative tetrameric tRNA splicing endonuclease [imported] - Guillardia theta nucleomorph
G190104

putative tetrameric tRNA splicing endonuclease [imported] - Guillardia theta
G190104

A,Note: a nucleomorph G111ardia theta
A,Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
G190104

R,Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001

A,Reference number: A99082; MUD:11323671; PMID:11323671

A,Accession: G90104

A,Accession: G90104

A,Retsidues: 1-242 < DOUA

A,Residues: 1-242 <
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Nature 408 1900, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F11P17.5 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C.Accession: C96638
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     Gaps
     10;
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     Indels
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Pred. No. 9.9;
4; Mismatches
4; Mismatches
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TKDCALAGFHGWTFL 429
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Matches 6; Conservative
          Conservative
                                                                                                                 4 CRIFAFHGWN--
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Best Local Similarity
Matches 9; Conserv
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A,Molecule type: DNA
A,Residues: 1-594 <STO>
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A, Genome: nucleomorph
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RESULT 15

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 28, 2004, 12:48:53 ; Search time 6.75 Seconds (without alignments) 154.282 Million cell updates/sec Run on:

US-10-069-056-9 120 1 TRACRIFAFHGWNYVKVCHA 20

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•			SUMMARIES		
Result		Query					
No.	Score	Match	Match Length	DB	ΩI	Description	tion.
٦	116	96.7	672	Н	VNCS MUMIV	4	뒽
8	115	95.8	668	ч	VNCS_PAVL3	P36311	parvovirus
М	113	94.2	672	ч	VNCS MUMIM	P07300	murine minu.
4	106	æ	672	ч	VNCS PAVHH	P03133	hamster par
ഗ	97	80.8	662	ч	VNCS PAVPK	P52502	
9	92	76.7	099	7	VNCS PAVPN	P18547	porcine par
7	91	75.8	392	٦	VNCS FPV	P06431	feline panl
æ	91	75.8	699	٦	VNCS FPV19	P24842	feline panl
o	91	75.8	668	-	VNCS MEVA	P27438	mink enteri
10	91	75.8	668	٦	VNCS PAVCN	P12929	canine parv
11	48	40.0	246	7	SIX6 HUMAN	095475	homo sapien
12	48	40.0	246	ď	SIX6 MOUSE		mus musculu
13	46	38.3	299	H	COAT HELVS	000556	helenium vi
14	46		2126	-	PKDR MOUSE	09z0t6	mus musculu
15	45.5	37.9	1310	-	A8B3_HUMAN		homo sapien
16	4.5		315	Н	COAT_CVB		chrysanthem
17	44	36.7	421		DCTA_BACSU		bacillus su
18	44	36.7	422	-	CHMO_ARATH		arabidopsis
19	44	36.7	507	Н			homo sapien
20	44	36.7	512	Н			mus musculu
21	44		512	-		063016	rattus norv
22	43.5	9	521	-	PGS1_YEAST	P25578	saccharomyc
23	43	S	282	-	Y32K_BNYVG	P19231	beet necrot
24	43	ů.	396	-		Q10002	caenorhabdi
25	43	'n.	491	Н	GLG2_SYNY3	P72623	synechocyst
56	43	35.8	571	Н	SYE_METMA	08pw52	methanosarc
27	43	35.8	2253	н	PKDR HUMAN	09ntg1	homo sapien
28	42.5	35.4	295	Н		092671	zymomonas m
59	2	35.4	521				вассратошус
30		35.4	1251		A8B1_HUMAN		homo sapien
31	42	35.0	238	-	ATE_SHEON		shewanella
32	42	35.0	293	7	COAT_PVSP		potato viru
33	42	35.0	363	٦	VP43_NPVAC	P34050	autographa

Q9ns82 homo sapien Q9jmh8 mus musculu P20386 kluyveromyc P98001 saccharomyc P00401 saccharomyc O57424 gallus gall Q8tt52 methanosarc Q03348 rattus norv P18433 homo sapien P18052 mus musculu Q9juc9 neisseria m	
AAA1 HUMAN AAA1 MOUSE COX1 KLULA COX1 SACDO COX1 SACDO COX1 SEAST HAS2 CHICK SYE METAC PTRA HUMAN PTRA MOUSE GLND NEIMB	
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523 5334 5344 552 796 796 802 852 852	
4 4 4 4 4 4 4 4 4 4 4 4 0 0 0 0 0 0 0 0	
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ALIGNMENTS

MUMIV STANDARD; PRT; 672 AA. WORSS MUMIV STANDARD; PRT; 672 AA. PRO3134; PRT; 672 AA. PRO3134; PRT; 672 AA. PRO3134; PRT; PRT; PRT; PRT; PRT; PRT; PRT; PRT	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Agtell C.R., Thomson M., Merchlinsky M., Ward D.C.; Agtell C.R., Thomson M., Merchlinsky M., Ward D.C.; "The complete DNA sequence of minute virus of mice, an autonomous parvovirus."; "The complete DNA sequence of minute virus of mice, an autonomous parvovirus.";	EMBL; J02275; AAA61109.1; EMBL; V01115; CAA24309.1; ALT_INIT. PIR, A00596; UTPUN. TRANSFAC; T02375; InterPro; IPR001257; Parvo_NS1. InterPro; IPR001257; Parvo_NS1; I. Nonstructural protein; Noncapsid protein; DNA replication; ATP-binding. ATP-binding. ATP-binding. SEQUENCE 672 AA; 76248 MW; 50298F27662E3CID CRC64; Local Similarity 95.0%; Pred. No. 1.5e-10; Local Similarity 95.0%; Pred. No. 1.5e-10; Local Similarity 95.0% o; Mismatches 1; Indels 0; Gaps 0; ITRACRIFAFHGWNYWCHA 20 ITRACRIFAFHGWNYWCHA 380	AA. .e)
672 AA. update) nn update 11 protei: us).	m., W. rus; virus; virus in ling in long in lo	IT. Protein; DNA r. (POTENTIAL). \$0298F27662E3C1D TE 116; DB 1; ad. No. 1.5e-10; Mismatches 1	668 A
D; PRT; 672 AA. Created) Last sequence update) Last annotation update) (Nonstructural protein urine parvovirus).	298737; cof minute 1018(1983) ary for vi the parve copyright. copyright. tutions as t is not r	ALT_INIT. ALT_INIT. NS1. 1. ATP (POTEN ATP (SOSPE27 ATP (SOTE 116; Pred: No. Pred: No. O: Mismatc CHA 20 CHA 380	D; PRT; 668 AA Created) Last sequence update)
STANDARD; (Rel. 01, Creat (Rel. 01, Last (Rel. 37, Last oten NS-1 (Non e virus (Murine NN viruses; Par 0794;	10.7.7. 341; Pubbmed=6 Thomson M., N. DNA sequence Res. 11:999- Seems necess Y: Belongs to Tentry is G Swiss Institute Broinformatic profit institute profit institute profit institute pries a licens institute pries a licens ail to licens	02275; AAA67109.1; 01115; CAA24309.1; ALT_I 3696, UVPVIM. C; T02375; Parvo_NS1. F01057; Parvo_NS1. F01057	STANDARD; (Rel. 29, Crea (Rel. 29, Last
NNCS_MUMIV ID VNCS_MUMIV STANDARD; PRT; 67 AC P03134; DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence upd DT 21-JUL-1986 (Rel. 37, Last annocation upd DT Noncapsid protein NS-1 (Nonstructural p SN NSI	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Astell C.R., Thomson M., Merchlinsky M., Ward "The complete DNA sequence of minute virus of parvovirus.", Nucleic Acids Res. 11:999-1018(1983). -!- FUNCTION: Seems necessary for viral DNA re!- SIMILARITY: Belongs to the parvoviruses no This SWISS-PROT entry is copyright. It is prod between the Swiss Institute of Bioinformatics the Buropean Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htte or send an email to license@isb-sib.ch).	EMBL; J02275; BAA67109.1; EMBL; V01115; CAA24309.1; ALT_INIT PIR, A03665; UTVUM. TRANSFAC; T02375; InterPro; IPR001257; Parvo_NS1. Pfam; PF01057; Parvo_NS1. Nonstructural protein; Noncapsid p; ATP-binding. NP BIND 399 406 ATP-Dinding. SEĞUENCE 672 AA; 76248 MW; 502; SEGUENCE 672 AA; 76248 MW; 502; Best Local Similarity 95.0%; Pred. Matches 19; Conservative 0; Milmatches 19; Conservative 0; Milmatches 19; Conservative 0; Milmatches 19; Conservative 0; Milmatches 11 TRACRIFAFHGWNYVKVCHA 20	LT 2 PAVL3 VNCS_PAVL3 P36311; 01-JUN-1994 01-JUN-1994
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhode S.L. III, Paradiso P.R.; "Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybrid-arrested translation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamster parvovirus H1.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                 Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X01457; CAA25689.1; -.
PIR; A03695; UYPVV1.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                    Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.3%; Score 106; DB 1; Length 67
85.0%; Pred. No. 5.5e-09;
Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 ATP (POTENTIAL).
75993 MW; 12F331142F72AA6D CRC64;
                                                                                                                                                                                                                                                          ATP (POTENTIAL).
I -> L (IN REF. 2).
25F025FB328B4DF0 CRC64;
                                                                                                                                                                                                                                                                                                                               94.2%; Score 113; DB 1;
90.0%; Pred. No. 4.4e-10;
iive 1; Mismatches 1;
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                                                                                                                                                EMBL; X02481; -; NOT ANNOTATED CDS. EMBL; M12032; AAA69567.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                              361 TRICKIFAFHGWNYVKVCHA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRACRIFAFHGWNYVKVCHA 20
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                                                                                                                                                                                    InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                             597 I
76140 MW;
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nes 18; Conservative
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672 AA;
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                                                                                                                                                                                                                                                              399
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"DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:367-1088).
-i- FUNCTION: Seems necessary for viral DNA replication.
-i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                             Virology 192:339-345(1993).
-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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MEDIINE=86115415; PubMed=3502703;
MEDIINE=86115415; PubMed=3502703;
MEDIINE=86115415; PubMed=3502703;
MEDIINE-86115415; PubMed=3502703;
MEDIINE-86115415; PubMed=3502703;
MIDA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                           Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI TaxID=35339;
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0
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10795;
                                                                                                                                                      MEDLINE-93297126; PubMed-8517025;
Diffeot N., Chen K.C., Bates R.C., Lederma M.;
The complete nucleotide sequence of parvoirus Lulli and
"The complete unique sequence possibly responsible for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 115; DB 1; Length 668;
Pred. No. 2.1e-10;
1; Mismatches 1; Indels
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P07300; P10837;
01-APR-1998 (Rel. 07, Created)
01-JUL-1998 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A44276; A44276. - - - PIGTAFPO, IPRO01257; Parvo NS1. PF01057; Parvo NS1; I. Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP (POTENTIAL).
CAE69049F8F86B53 CRC64;
           15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
         annotation update)
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668 AA; 75846 MW;
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                               encapsidation pattern.
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                                                                   Parvovirus LuIII.
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Gaps

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complete nucleotide sequence of an infectious clone of porcine
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SEQUENCE FROM N.A.
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ID _VNCS_FPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=96183900; PubMed=8642680;

MEDLINE=96183900; PubMed=8642680;

MEDLINE=1000 of the Aresse strain of porcine parvovirus:

"Genome organization of the Kresse strain of porcine parvovirus:
identification of the allotropic determinant and comparison with
those of NADL-2 and field isolates.";
J. Virol. 70:2508-2515(1996).

-I- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                   Porcine parvovirus (strain Kresse) (PPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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VCBI_TaxID=10797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 80.8%; Score 97; DB 1; Length 662; Local Similarity 70.0%; Pred. No. 1.4e-07; es 14; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91021005; PubMed=2219713;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 405 ATP (POTENTIAL).
662 AA; 75591 MW; B53F76D9F9FBD613 CRC64;
                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last amotation update)
Noncapsid protein NS-1 (Nonstructural protein NSI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNCS_PAVPN STANDARD; PRT; 660 AA. P18547; P22965; D180V-1990 (Rel. 16, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 01-AUG-1998 (Rel. 37, Last annotatio
                                                                                                                                662 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porcine parvovirus (strain NADL-2) (PPV).
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Pfam; PF01057; Parvo NS1; 1.
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                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=73487;
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                                                                                                                             PAVPK
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                                                                                                    SEQUENCE OF 367-660 FROM N.A.
MEDLINE=90085785; PubMed=2596019;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
Valcotide sequence analysis of the capsid genes and the right-hand terminal palindrome of porcine parvovirus, strain NADL-2.";
Virology 173:368-377(1989).
-i. FUNCTION: Seams necessary for viral DNA replication.
-i. SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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K -> R (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNTDT -> NLHLTPTPPDSAIRTP (IN
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.7%; Score 92; DB 1; Length 660; 65.0%; Pred. No. 8.3e-07; Live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nonstructural protein; Noncapsid protein; DNA replication;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660 AA; 75300 MW;
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parvovirus, strain NADL-2."
Virology 178:611-616(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 65.0
Matches 13; Conservative
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- FUNCTION: Seems necessary for viral DNA replication.
-1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martyn J.C., Davidson B.E., Studdert M.J.;
"Nucleotide sequence of feline panleukopenia virus: comparison with
canine parvovirus identifies host-specific differences.";
J. Gen. Virol. 71:2747-2753(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mapping specific functions in the capsid structure of canine
parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feline panleukopenia virus (strain 193) (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Created)
1-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 91; DB 1; Length 392; 65.0%; Pred. No. 7.1e-07; tive 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                              124 131 ATP (POTENTIAL).
392 AA; 43971 MW; B875ADDB4977F616 CRC64;
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                                                                                           EMBL; M10824; AAA47160.1; -.
PIR; A03697; UYPV1F.
InterPro; IPR0013593; AAA ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; T.
SMART; SM00392; AAA, 1.
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PIR; A36608; UYPVFP.
InterPro; IRR003593; AAA ATPase.
InterPro; IRR001257; Parvo NS1;
Pfam; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
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VNCS_FPV19
ID _VNCS_FPV19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Construction and nucleotide sequence analysis of an infectious DNA clone of the autonomous parvovirus, mink enteritis virus.";
J. den. Virol. 72:867-875(1991).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                  Gaps
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Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.,
                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mink enteritis virus (strain Abashiri) (MEV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                           75.8%; Score 91; DB 1; Length 668; 65.0%; Pred. No. 1.2e-06; live 4; Mismatches 3; Indels
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01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nonstructural protein; Noncapsid protein; DNA replication;
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407 ATP (POTENTIAL).
23 N -> D (IN REF. 2).
443 I -> V (IN REF. 2).
5755 I -> N (IN REF. 2).
76768 MW, 4F8FEA3EE62D2AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 407 ATP (POTENTIAL).
668 AA; 76736 MW; DBD5F9E92113685C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 91; DB 1; 165.0%; Pred. No. 1.2e-06; tive 4; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          668 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 12, Created)
(Rel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                 362 SRTCQIFRMHGWNWIKVCHA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D00765; BAA00662.1; -. PIR; A38350; UYPVME.
                                                                                                                                                                                    65.0%;
                                                                                                                                                                                    Local Similarity 65.0 es 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goto H., Shinagawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                       668 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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WCS_PAVCN

ID WCS_PAVCN

AC P12929;

DT 01-OCT-1989 (1)

DT 01-OCT-1989 (1)
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                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
VNCS MEVA
ID VNCS MEVA
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us-10-069-056-9.rsp

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TRANSFAC; T03279
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SIX6 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
SIXA HUMAN
SIXALLANDARL,
O95475; O9PIX8;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein SIX6 (Sine oculis homeobox homolog 6) (Optic homeobox protein Drotein OPTX2).
1 (Homeodomain protein OPTX2).
2) (Homeodomain protein OPTX2).
3 IX6 OR OPTX2 OR SIX9.
3 SIX6 OR OPTX2 OR SIX9.
4 SIX6 OR OPTX2 OR SIX9.
5 SIX6 OR OPTX2 OR SIX9.
                                                                                                                                                                                                                                                                                                                                                        Parrish C.R.;
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                           MEDLINE=88062992; PubMed=2824850;
Reed A.P., Jones E.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE-99310672; PubMed=10381575;
Loez-Rios J., Gallardo M.E., Rodriguez de Cordoba S., Bovolenta P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Eye;
Leppert G.S., Yang J.-M., Toy J., Sundin O.H.;
"OFTX2, a novel gene expressed in the eye, belongs to a cluster of
sine oculis-related homeobox genes.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                             Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBL_TaxID=10791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91; DB 1; Length 668; Pred. No. 1.2e-06; 3; Indels 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76764 MW; DE2CCEA69D2A63A6 CRC64;
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NSI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M19296; AAA67459.1; --
EMBL, M38245; AAB02798.1; --
EMBL; A22962; UTPVCP.
InterPro; IPR001593; AAA_ATPase.
InterPro; IPR001527; Parvo NS1.
Ffam; PF01057; Parvo NS1.
SMART; SM00382; AAA; I.
                                                                           (strain N) (CPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 SRTCOIFRMHGWNWIKVCHA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.8%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 65.0 es 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                              Canine parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400
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                                                                                                                                                                                                                                         Gallardo M.E., Lopez-Rios J., Fernaud-Espinosa I., Granadino B., Sanz R., Ramos C., Ayuso C., Seller M.J., Brunner H.G., Bovolenta P., Rodriguez de Cordoba S., "Genomic cloning and characterization of the human homeobox gene SIX6 reveals a cluster of SIX genes in chromosome 14 and associates SIX6 hemizygosity with bilateral anophthalmia and pituitary anomalies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Silver project.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCIION: May be involved in eye development.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUB SPECIFICITY: Expressed in the developing and adult retina.
Also expressed in the hypothalamic and the pituitary regions.
-!- SIMILARITY: Belongs to the SIX/Sine oculis homeobox family.
-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
"Six9 (Optx2), a new member of the six gene family of transcription factors, is expressed at early stages of vertebrate ocular and oltuleary development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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DNA BIND 128 187 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 48; DB 1; Length 246; 55.6%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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246 AA; 27664 MW; 1A5FA3F57A76BC77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0007397; P:histogenesis and organogenesis; TAS. GO; GO:0007601; P:vision; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
InterPro; IPR007105; SIX.
InterPro; IPR007106; SIX_SINE_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-165 FROM N.A.
Kitano T., Kobayakawa H., Saitou N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=99443875; PubMed=10512683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF031648; AAF04402.1; -.
EMBL, AA011785; CAA09773.1; -.
EMBL, AF141651; AAD49844.1; -.
EMBL, AB041399; BAA94484.1; -.
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PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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090228; 088423;
28-FEB-2003 (Rel. 41, Created)
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55 RARAIVAFHGGNYRELYH
                                                                              pituitary development.";
Mech. Dev. 83:155-159(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 61:82-91(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P41778; 1DU6.
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Gaps

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092076;
28-FEB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Polycystic kidney disease and receptor for egg jelly related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Cost protein (Capsid protein).
Helenium virus S (HelVS).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=90362082; PubMed=2391504;
Foster G.D., Millar A.W., Meehan B.M., Mills P.R.;
"Nucleotide sequence of the 3'-terminal region of Helenium virus S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the potexviruses coat protein family.
  PROSITE; PS50071; HOMEOBOX 2; 1.
Developmental protein; Homeobox; DNA-binding; Nuclear protein.
DNA BIND 126 186 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Gen. Virol. 71:1877-1880(1990).
                                                                                                                                                                                    40.0%; Score 48; DB 1; Length 246; 55.6%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.3%; Score 46; DB 1; Length 299; 43.8%; Pred. No. 5.8;
                                                                            141 H -> N (IN REF. 3).
220 S -> T (IN REF. 3).
27741 MW; F1332D5E617B2CF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 AA; 32877 MW; ED7E43D54CB20BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 AA.
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PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, D10454; BAA01248.1; -- interPro. PRO0052; Plrvir_coat. Pfam, PF00286; virus P-coat. PRINTS; PR00232; POTXCARLCOAT.
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55 RARAIVAFHGGNYRELYH 72
                                                                                                                                                                                                                                                                                         2 RACRIFAFHGWNYVKVCH 19
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187 RVCRLYAPVTWNYMHI 202
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                                                                                                                                                                                                            Local Similarity 55.6
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 43.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                          186
141
220
                                                                                                                                 246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=12171;
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SEQUENCE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAT HELVS
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                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

STRAIN=BALB/c; TISSUE=Embryonic head;
MEDLINE=9910672; PubMed=10381575;
Lopez-Rios J., Gallardo E., Rodriguez de Cordoba S., Bovolenta P.;
"Six9 (Optx2), a new member of the Six gene family of transcription factors, is expressed at early stages of vertebrate ocular and factors, is expressed at early stages of vertebrate ocular and mech. Dev. 83:155-159(1999).

T pituitary development.";
Mech. Dev. 83:155-159(1999).

- I- FUNCTION: May be involved in eye development.

- SUBCELLUIAR LOCATION: Nuclear (By similarity).

- ITSSUE SPECIFICITY: In the developing embryo, expressed mainly in the ventral optic stalk, optic chiasma, the neural retina and the primordial tissues that give rise to the pituitary/hypothalamus axis. Not expressed in the lens placede.

- DEVELOPMENTAL STAGE: Expression is first detected in the embryo at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license@isb-sib.ch/announce/or send an email to license@isb-sib.ch).
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein SIX6 (Sine oculis homeobox homolog 6) (Optic homeobox
                                                                                                                                                                                                                                                                              STRAIN=C57BL/6;
MEDLINE=98393698; PubMed=9724757;
TOY J., Yang J.-M., Leppert G.S., Sundin O.H.;
The Optx2 homeobox gene is expressed in early precursors of the eye and activates retina-specific genes.";
Proc. Natl. Acad. Sci. U.S.A. 95:10643-10648(1998).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jean D., Bernier G., Gruss P.;
"Six6 (Optx2) is a novel murine Six3-related homeobox gene that
demarcates the presumptive pituitary/hypothalamic axis and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the SIX/Sine oculis homeobox family. SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF050130; AAC33850.1; -.
EMBL; AF135267; AAD48911.1; -.
EMBL; AA011787; CAA09775.1; -.
EMBL; AK017544; -; NOT_ANNOTATED_CDS.
HSSP; P40424; 1872.
TRANSFAC; T03272; -.
MGD; MG1:1341840; Six6.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:0005515; F:protein binding; IPI.
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SMART; SM0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
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InterPro; IPR0010047; HTH lambrepressr.
InterPro; IPR007106; SIX_SINE_homeo.
InterPro; IPR007106; SIX_SINE_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99400097; PubMed=10473118;
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ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mech. Dev. 84:31-40(1999).
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                                                                                                  SIX6 OR SIX9 OR OPTX2. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ventral optic stalk.
                                                                               protein).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=10090;
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Gaps

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Indels

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                      MEDLINE-99138702; PubMed-9949214;
MEDLINE-99138702; PubMed-9949214;
Hughes J., Ward C.J., Aspinwall R., Butler R., Harris P.C.;
Hughes J., Ward C.J., Aspinwall R., Butler R., Harris P.C.;
"Identification of a human homologue of the sea urchin receptor for egg jelly: a polycystic kidney disease-like protein.";
Hum. Mol. Genet. 8:543-549(1999).
-!-FUNCTION: May have a central role in fertilization. May generate a Ca(2+) transporting channel directly involved in initiating the acrosome reaction of the sperm.
-!-SUBUNIT: May form homomultimers or heteromultimers in combination with an as yet unidentified subunits.
-!- DEVELOPMENTAL STAGE: Expression begins at about 2 weeks and continues into adult life, mirroring the production of mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYCYSTIC KIDNEY DISEASE AND RECEPTOR FOR EGG JELLY RELATED PROTEIN. EXTRACELLULAR (POTENTIAL).
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Ionic channel; Signal; Glycoprotein; Transmembrane.
SIGNAL 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the polycystin family.
-!- SIMILARITY: Contains 1 PLAT domain.
-!- SIMILARITY: Contains 1 REJ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD, MGI.1338786; Pkdrej.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR002821; Ion_trans.
InterPro; IPR002821; Ion_trans.
InterPro; IPR002859; PkD/REJ-IIke.
InterPro; IPR003859; PkD/REJ-IIke.
InterPro; IPR003859; PkD/REJ-IIke.
InterPro; IPR003876; PLAT_LHZ.
InterPro; IPR00876; PLAT_LHZ.
Pfam; PF00520; ion_trans; I.
Pfam; PF00210; REJ; I.
Pfam; PF00210; REJ; I.
PRINTS; PR01433; POLYCYSTINZ.
SMART; SM00308; ILEZ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement ( or send an email to license@isb-sib.ch)
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precursor (PKD and REJ homolog)
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875
896
                                Mus musculus (Mouse)
                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                  spermatozoa.
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POTENTIAL. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). REJ. N-LINKED (GLCNAC) (POTENTIAL).	Score 46; DB 1; Length 2126; Pred. No. 39; ;; Mismatches 6; Indels 0; Gaps	RESULT 15 A8B3 HUMAN STANDARD; PRT; 1310 AA. A606423; Q81048; Q966M2; DT 30-MAY-2000 (Rel. 39, Created) T 10-OCT-2003 (Rel. 42, Last sequence update) DT 10-OCT-2003 (Rel. 42, Last annotation update) DE 10-OCT-2003 (Rel. 42, Last annotation update) DE 10-OCT-2003 (Rel. 42, Last annotation update) DT 10-OCT-2003 (Rel. 42, Last annotation update) DE 10-OCT-2003 (Rel. 42, Last ann	J.W., Green E.D., Dickson M.C., J., Schmutz J., Myers R.M., Winski M.I., Skalska U., Smailus D.E., Jones S.J.M., Marra M.A.; analysis of more than 15,000 full-length human ";
FT TRANSMEM 1965 1985 FT DOMAIN 1986 2019 FT TRANSMEM 2020 2040 FT DOMAIN 2041 2126 FT DOMAIN 102 796 FT DOMAIN 1114 1231 FT CARBOHYD 94 94 FT CARBOHYD 129 129 FT CARBOHYD 243 243 FT CARBOHYD 243 243 FT CARBOHYD 243 243 FT CARBOHYD 774 774 FT CARBOHYD 774 774 FT CARBOHYD 776 776 FT CARBOHYD 776 776 FT CARBOHYD 1063 1063 FT CARBOHYD 1063 1063 FT CARBOHYD 1063 1063 FT CARBOHYD 1607 1607 FT CARBO	Query Match 38.3%; Best Local Similarity 46.7%; Matches 7; Conservative 2 Qy 6 IFAFHGMNYVKVCHA 20 : Db 1983 VFGQHEWNYSNMIHA 1997	RESULT 15 A8B3 HUMAN ID A8B3 HUMAN STANDARD; PRT; 1310 AA. AC 060423; Q&IVB8 Q&RAY8 QS6M22; DT 10-OCT-2003 (Rel. 39, Created) DT 10-OCT-2003 (Rel. 42, Last sequence update) DT 10-OCT-2003 (Rel. 42, Last sequence update) DE class I type 8B member 31. GN ATPBB3 OR ATPIK OR FOS37502_2. OC Mammalia; Eutheria; Primates; Catarrhini; Hom OR Sapiens (Human). OC Mammalia; Eutheria; Primates; Catarrhini; Hom OR Sapiens (Human). RP SEQUENCE FROM N.A. (ISOFORM 2). RN NISURE-Eye, and Testis; Primates; Catarrhini; Hom OR Sapiens (Russelle St.). Feathed-12477932; RA Alschul S.F., Feathed-12477932; RA Alschul S.F., Collins F.S., Wagner L., Shenm RA Alschul S.F., Jordan H., Moore T., Max S. I., Rabistensko, L., Marusina R., Peters G.J., Abram RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Cara RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Cara RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Cara RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Male R. Raha S.S., Loquellano N.A., Peters G.J., Abra RA Brobards S.A., McEwan P.J., McKernan K.J., Male R. Villaldn D.K., Muzny D.M., Sodergen B.J., Lu RA Frichards S., Worley K.C., Hale S., Garcia A.M. RA Frey Williang M., Madan A., Young A.C., Shevchenko, S.A., McKen M., Sodergen B.J., Lu RA Whiting M., Madan A., Young A.C., Shevchenko.	RA Blakesley K.W., Touchman J.W. RA Rodriguez A.C., Grimwood J., RA Butterfield Y.S.N., Krzywinsk RA Schnerch A., Schein J.E., Jon RT "Generation and initial analy RT and mouse cDNA sequences."; PT. Drog Nafl Arad Sching R
		C MAC	···,

EXTRACELLULAR (POTENTIAL)

POTENTIAL.

452 005 026 038 058 088 110

RANSMEN RANSMEN

DOMAIN OMAIN OMAIN

DOMAIN TRANSMEM

TRANSMEM

CYTOPLASMIC (POTENTIAL).

POTENTIAL

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Damerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
"Sequence analysis of a 3.5 Mb contig in human 19913.3 containing a
                                                                                                                                                                                                                               Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Yishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma I Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                             serine protease gene cluster.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished observations (FEB-2003).
Unpublished observations (FEB-2003).
-I- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                CONCEPTUAL TRANSLATION (ISOFORM 1)
[2]
SEQUENCE OF 173-1310 FROM N.A.
                                                                                                                                                                                                       SEQUENCE OF 978-1310 FROM N.A.
                                                                                                                                                                                                                       rissum=Testis;
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completed: May 28, 2004, 12:57:42
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5 RIFAFHG-WNYVKVC 18 Conservative

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Best Local Similarity
Matches 7; Conserv

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Gaps

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37.9%; Score 45.5; DB 1; Length 1310; 46.7%; Pred. No. 29; tive 4; Mismatches 3; Indels 1

148029 MW; F1A1C25A8DE696FC CRC64;

1310 AA;

SEQUENCE Query Match

VARSPLIC

FTIG=VSP

Missing

PHOSPHORYLATION (BY SIMILARITY). MAGNESIUM (BY SIMILARITY). MAGNESIUM (BY SIMILARITY).

(in isoform 2) 007304

CYTOPLASMIC (POTENTIAL)

POTENTIAL. EXTRACELLULAR (POTENTIAL)

145 151 172 192 217

1123

TRANSMEM

'RANSMEM

1089

1146 1152 1173 1193 1218 495

'RANSMEN MOD RES DOMAIN

DOMAIN

949

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL) POTENTIAL. CYTOPLASMIC (POTENTIAL).

7.75 secs Search comp Job time :

collaboration

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or send an email to license@isb-sib.ch).

EMBL; BC033179; AAH33179.1; ALT SEQ. EMBL; AC004755; AAC17601.1; ALT SEQ. EMBL; AK057452; BAB71492.1; ALT INIT

HGNC:13535; ATP8B3

Genew:

605866;

MIM;

EMBL; BC035162; AAH35162.1; -.

InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR006539; Flippase.
InterPro; IPR0119; CATATPASE.
TIGRPAMs; TIGR0162; ATPase.-Plipid; 1.
PROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;

POTENTIAL. EXTRACELLULAR (POTENTIAL)

CYTOPLASMIC (POTENTIAL)

EXTRACELLULAR (POTENTIAL)

POTENTIAL.

RANSMEM

DOMAIN DOMAIN

TRANSMEM DOMAIN *IRANSMEM*

Isold=060423-2; Sequence=VSP 007304; SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
CAUTION: Ref.1 (AAM33179) sequence differs from that shown due to presence of unspliced intronic sequence in the C-terminus.
CAUTION: Ref.2 sequence differs from that shown due to erroneous

gene model prediction.

-

IsoId=060423-1; Sequence=Displayed;
Note=No experimental confirmation available;

Name=2

Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

Database

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Q84193 canine park
P89514 feline park
P89514 feline park
Q18097 caenorhabdi
Q9462 drosophila
Q8876 lactobacill
Q88102 drosophila
Q81186 drosophila
Q97217 helicobacte
Q97219 pongo pygma
Q9729 pongo pygma
Q9729 pongo pygma
Q9729 pongo pygma
Q9723 arabidopsis
Q9789 pondetella
Q77013 bordetella
Q77013 bordetella
Q9780 drosophila
Q9790 drosophila
Q9781 caenorhabdi
Q8786 drosophila
Q9786 drosophila
Q9786 caenorhabdi
Q8786 caenorhabdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MVM(p);
MEDILINE=87061199; PubMed=3783817;
MEDILINE=87061199; PubMed=3783817;
MOTGAIN W. R., Mard D. C.;
"Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs.";
J. Virol. 60:1170-1174 (1986).
EMBL; J02275; AAA67108.1;
P89512 feline
P90484 feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MVM(p);
MEDLINE=86115415; PubMed=3502703;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M., Ward D.C.; virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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Last annotation update)
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MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky
"The complete DNA sequence of minute
                                                                                                                                                                  Q9N2A0
Q9N299
Q22723
Q9AW86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parvovirus.";
Nucleic Acids Res. 11:999-1018(1983)
                           Q84393
P89514
Q18097
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Q9N6V2
Q88W76
                                                                                                             Q8ING2
Q8IH86
Q9ZJY7
Q9N2A1
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Q7W1A9
Q7WUE3
Q9VEC2
Q9V9Y0
Q9DES7
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Q8C0Z9
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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J. Virol. 57:656-669(1986)
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Nonstructural protein.
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Q84363 murine minu
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197.199 Million cell updates/sec
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                                                                                               May 28, 2004, 12:52:08 ; Search time 32 Seconds
             GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
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1 TRACRIFAFHGWNYVKVCHA 20
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_plant:*
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Maximum DB seq length: 200000000
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Rat parvovirus type 1: the prototype for a new rodent parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Yale;
MEDLINE=21102993; PubMed=11172095;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
"Divergent replication kinetics of two phenotypically different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                     Autonomous rat parvovirus RV-Y.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=155025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98184569; PubMed-9525656;
Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 397;
                                 Length 672;
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672 AA; 76112 MW; 31C6365276727363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Nonstructural protein 1 (Fragment).
                             93.3%; Score 112; DB 12;
85.0%; Pred. No. 9e-09;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.3%; Score 106; DB 12;
85.0%; Pred. No. 4.4e-08;
iive 1; Mismatches 2;
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                                                                                                                                                                                                                        PRT;
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EMBL; AF317513; AAK27438.1; -.

InterPro; IPR001257; Parvo NS1.

Pam, PF01057; Parvo NS1; J.

NON TER

SEQUENCE 397 AA; 43959 MW; D620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serogroup.";
J. Virol. 72:3289-3299(1998).
EMBL; AF036711; AAC40695.1; -.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
NON_TER
                                                                                                                      361 TRTCKIFAFHGWNYIKVCHA 380
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                                                                                                    1 TRACRIFAFHGWNYVKVCHA 20
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Best Local Similarity 85.0°
                               Query Match
Best Local Similarity 85.0 Matches 17; Conservative
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                                                                                                                                                                                                                        PRELIMINARY;
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Ball-Goodrich L.J., Johnson B.;
"Molecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                        Gaps
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MEDLINE=86115415; PubMed=3502703;
MEDLINE=86115415; PubMed=3502703;
MEGLI C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                NS1.
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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NCBI_TaxID=35340;
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U12469; ABAG1405.1; J.
InterPro; IFR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prototype strain.";
J. Virol. 570.856-669(1986).
J. Virol. 570.856-669(1) -.
PIR; A23008; UYPVIM.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
Pfam; PF01057; Parvo NS1, 38063 MW; 9F029C327C7F4BBF CRC64;
 Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 721 AA; 91896 MW; 18391758E42F0DCF CRC64;
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Last annotation update)
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Pred. No. 2.4e-09;
                                            96.7%; Scor.
95.0%; Pred. No. 2...
0; Mismatches
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                        Local Similarity 95.0
nes 19; Conservative
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es 18; Conserv
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01-JUN-2003
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Matches

RESULT 3 Q83429

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.3%; Score 106; DB 12; Length 672; Best Local Similarity 85.0%; Pred. No. 7.4e-08; Matches 17; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence of a Diabetogenic Parvovirus of Rats.";
Submitted (NOV.1996) to the EMBL/GenBank/DDBJ databases.
EMBL, '199033; AAB38326.1; -.
InterPro: IPRO10FR01257; Parvo NS1.
Pfam: PF010F7; Parvo NS1; I.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
EMBL; A3212130; AAM93272.1; -.
InterPro; IPRO157; Parvo NS1.
Pfam; PF01057; Parvo N31; I.
SEQUENCE 672 AA; 75987 MW; 22B4611C20CDB6E9 CRC64;
                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                672 AA.
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                                                                                                                                                              Created)
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01-OCT-2002 (TrEMBLrel. 22, Created)
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                                                                                                                    PRT;
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  361 TRICRIFAEHGWNYIKVCHA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 TRTCRIFAEHGWNYIKVCHA 380
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                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Nonstructural protein 1.
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Best Local Similarity 85.03
Matches 17; Conservative
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                                                                                                                  PRELIMINARY;
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Brown D.W., Like A.A.;
                                                                                                                                                                                                                                Non-capsid protein
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                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=12441;
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                                                                                                                                                                                                                                                                            Kilham rat virus.
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Q8JV14
ID Q8JV14
AC Q8JV101
DT 01-OC
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Q8JV28
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=74581;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172385;
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88.3%; Score 106; DB 12; Length 672;
Best Local Similarity 85.0%; Pred. No. 7.4e-08;
Matches 17; Conservative 1; Mismatches 2; Indels 0;
88.3%; Score 106; DB 12; Length 665; 85.0%; Pred. No. 7.4e-08; ive 1; Mismatches 2; Indels
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MEDLINE=99184569; PubMed=9525656;
Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

BEDLINE=22120170; PubMed=12124471; Man C.H., Solution D.J., Riley L.K.; Wan C.H., Solution of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parvoviruses.";
J. Gen. Virol. 83.2075-2083(2002).
EMBL; AF332882; AAM; A375.1; -:
InterPro; IFR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
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J. Virol. 72:3289-3299(1998).

EMBL; AF036710; AAC40693.1; -.
InterPro; IPR001257; Parvo_NSI.
Pfam; PF01057; Parvo_NSI; I.
Pfam; PF01057; Parvo_NSI; I.
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                    354 TRTCRIFAEHGWNYIKVCHA 373
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                                                                                           1 TRACRIFAFHGWNYVKVCHA 20
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                                              17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Nonstructural protein
  Query Match
Best Local Similarity
Matches 17; Conserv
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Q8JV18 RESULT 7 Q8JV18

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Evolutionary pattern of feline panleukopenia virus differs from that
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                                                                                          "Evolutinary pattern of feline panleukopeina virus differs that of
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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                                                                                                                             canine parvovirus.";
submitted (DEC-1996) to the EWBL/GenBank/DDBJ databases
EMBL, ARD000065: PAA19023.1;
GO; GO; 0000166; F: muclectide binding; IEA.
InterPro; IPR00159; AAA_ATPase.
InterPro; IPR001257; Parvo NS1.
FFam; PF01057; Parvo NS1; T.
SMART; SM00322; AAA, 1.
SMART; SM00322; AAA, 1.
SEQUENCE 668 AA; 76755 MW; 37ABDFD347017F52 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nonstructural protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.8%; Score 91; DB 12; 65.0%; Pred. No. 1.4e-05; iive 4; Mismatches 3;
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nes 13; Conservative
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FROM N.A.
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                                                              Horiuchi M.;
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Horiuchi M.;
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P89515;
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P90449
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                                                                                                            Rat minute virus 1c.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=172387;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172386;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
NCBI_TaxID=10786;
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22120170; PubMed=12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-22120170; MEDLINE-22120170; Venermo M., Pintel D.J., Riley L.K.; Wan C.H., Socilund-Venermo M., Pintel D.J., Riley L.K.; "Molecular characterization of three newly recognized rat
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EMBL; AF332883; AAM93277.1; -.
InterPro; IFRO01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 76201 MW; C2F1A71F6EF449A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
EMBL; AF312884; AAM93279.1; -.
InterPro; IPRO01257; Parvo NS1.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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Pred. No. 7.4e-08;
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88.3%; Score 106; DB 12;
Best Local Similarity 85.0%; Pred. No. 7.4e-08;
Matches 17; Conservative 1; Mismatches 2;
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Best Local Similarity 85...
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Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AB000069; BAA19030.1; ---

EMBL; AB000063; BAA19030.1; ---

GO; GO:0019012; C:virion; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

InterPro; IPR001557; Parvo NS1.

R SMART; SMO01557; Parvo NS1; I.

SMART; SMO01382; AAA; I.

R SMART; SMO01382; AAA; I.

NOMBERUCEURAL PROCEGIN.

SEQUENCE 668 AA; 76769 MW; OECAFEGBF62ASDE0 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ORGANISM: Enterococcus faecium
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Sequence 5660, Ap
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Sequence 11, Appl
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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44444444444444444444444444444444444444	532A-5548 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	APPLICATION FILING DATE ATTORNEY/AGENT I NAME: Arini REGISTRATIO TELECOMMULCATIO TELEPAX: (7 INFORMATION FOR SEQ I SEQUENCE CHARACT LENGTH: 79 TYPE: amino TOPOLOGY: 1 MOLECULE TYPE: amino TOPOLOGY: 1 MOLECULE TYPE: ANINO HYPOTHETICAL: YE ORIGINAL SOURCE: CREATER ORIGINAL SOURCE: ORIGINAL SOURCE:
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; Sequence 6, Application US/08736723A
; Sequence 6, Application US/08736723A
; GENERAL INFORMATION:
    APPLICANT: SUDA, NARUSHI
; APPLICANT: TIOGA, YUTAKA
; TITLE OF INVENTION: FOR DETECTING THE SAME
; TITLE OF INVENTION: FOR DETECTING THE SAME
; NUMBER OF SEQUENCES:
    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
    ADDRESSEE: P.C.
    STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
    CITY: ALINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2; Length 306;
Pred. No. 32;
  Length 79;
                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/736,723A
FILING DATE: 25-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-302297
FILING DATE: 27-0CT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-352285
FILING DATE: 27-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REFERENCE/DOCKET NUMBER: 2589-042-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 6, Application US/09221114A; Patent No. 6132960; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.7%;
Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||::| |||:
197 RVCRLYAPLTWNYM 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RACRIFAFHGWNYV 15
                                                                                2 RACRIFAFHGWNYV 15
                                                                                                                        19 KMCRLFIYHGKNVV 32
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                    RESULT 2
US-08-736-723A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-221-114-6
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Sequence 11397, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11397
LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1429, Application US/09489039A

Sequence 1429, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICADIT GALY Breton et. al
APPLICADITON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001

CURRENT PILING DATE: 2000-01-29

RIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

RIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 14279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
APPLICANT: HATAYA, TATSUZI
TITLE OF INVENTION: GENE OF THE HOP LATENT VIRUS AND METHODS FOR DETECTING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 2580-0068-0DIV
CURRENT APPLICATION NUMBER: US/09/221,114A
CURRENT APPLICATION NUMBER: US/09/221,114A
EARLIER APPLICATION NUMBER: 08/736,723
EARLIER FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VEr. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 3; Length 306;
Pred. No. 32;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Score 44; DB 4; Length 388; 100.0%; Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14279
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||::| |||:
197 RVCRLYAPLTWNYM 210
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Hop latent viroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RACRIFAFHGWNYV 15
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BOUMANII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBSTRATE TRAPPING PROTEIN TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOPTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION A378:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         Score 42; DB 4
Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 49;
2; Mismatches
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Best Local Similarity 47.1%; Pred. No. 4
Matches 8; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/08685992
Patent No. 5912138
GENERALINFORMATION:
APPLICANT: TONES, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: TYROSINE PHOSPH
ITLIE OF INVENTION: TYROSINE PHOSPH
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         , ORGANISM: Acinetobacter baumannii
US-09-328-352-5612
                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 ACDVVDMEGYALAKVCH 145
                                                                                                                                                                                                                                                                                                                                                                                                            3 ACRIFAFHGWNYVKVCH 19
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TELECOMMUNICATION INFORMATION
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: HAMILTON, BROOT TWO Militia Drive
                                                                                                                                                                                                                                                                                                                      Query Match 35.0%;
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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      6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-685-992-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
      Patent No.
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                                                                                                                                                                                                                                                                    Sequence 4915, Application US/09543681A

Patent No. 6605709

GENERAL INCRMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: UNMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT PILING DATE: 1999-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

LEMSTH. 907
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Patent No. 6605709

GENERAL INPORMATION:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: US/09/543,681A

FILE REFERENCE: 2709.1002-001

CURRENT FPLING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION OF SEQUENCE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5660

LENGTH: 295
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                                                               Score 43; DB 4; Length 203;
Pred. No. 30;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 4; Length 897;
Pred. No. 1.3e+02;
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Pred. No. 52;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                  2 RACRIFAFHGW----NYVKVCHA 20
                                                                                                                                                                          63 RACRMSSPTGWYLLQALISACHA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 5612, Application US/09328352
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70 ACQLGIMYLFVFHAYNYLTV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ACR----IFAFHGWNYVKV 17
, ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11397
                                                               Query Match 35.8%;
Best Local Similarity 39.1%;
Matches 9; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 35.4%;
Similarity 40.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||| :||
292 IFAGAGWNVIKV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.8
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-543-681A-5660
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US-09-328-352-5612
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0; Gaps
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Sequence 11, Application US/09280597

Patent No. 668206

GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: SAP, Jan M.
TITLE OF INVENTION: PHOSPHATASE-ALPHA
ITILE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF SEQUENCE: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STREET: 1155 AVENUE OF THE AMERICAS
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,985
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
TELEPRANIS (212) 790-9090
TELEPRAN: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.0%; Score 42; Best Local Similarity 47.1%; Pred. No. Matches 8; Conservative 2; Mismatc
1155 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,985
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 SRQIRQFHFHGWPEVGI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRACRIFAFHGWNYVKV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                 STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-015-985-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: PHOSPHATASE-ALPHA
INUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                 Sequence 27, Application US/09144925

Patent No. 5951979

GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Tonks, Nicholas
APLICANT: Tilit, Andrew J.
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/685,992
FILING DATE: July 25,1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08015985
Patent No. 5538886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 SRQIRQFHFHGWPEVGI 191
                                                                               175 SRQIRQFHFHGWPEVGI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRACRIFAFHGWNYVKV 17
                                1 TRACRIFAFHGWNYVKV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: peptide US-09-144-925-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Mil:
CITY: Lexington
                                                                                                                                                                 RESULT 10
US-09-144-925-27
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Pred. No. 1.6e+02;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Sep, Jan M.
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
ZUNTRY: U.S.A.
ZIP: 10036
                                           CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: COLUZZI, LGULTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.0%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,985
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09280597
Patent No. 6682905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| | | |||| | :
677 SRQIRQFHFHGWPEVGI 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A. 742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 761
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRACRIFAFHGWNYVKV 17
                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.0%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       : 793 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 793 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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                               FILING DATE:
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TELEFAX: (
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US-09-540-236-2794

US-09-540-236-2794

Sequence 2794, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION UNMER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840
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Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.0%; Score 42; DB 35.7%; Pred. No. 68; Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                               2; Mismatches
INFORMATION:
(212) 790-9090
TELEX: (212) 869-9741/8864
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: 8; ...
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/015,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08015985 Patent No. 5538886
                                                                                                                                                                                                                                                                                                                                                                                                             129 SRQIRQFHFHGWPEVGI 145
                                                                                                                                                                                                                                                                                                                                                                         1 TRACRIFAFHGWNYVKV 17
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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90 CVVYCVAGWSFIKV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                  TOPOLOGY: unknown;
MOLECULE TYPE: protein
US-09-280-597-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: M.catarrhalis
US-09-540-236-2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-015-985-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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0; Gaps Best Local Similarity 47.1%; Pred. No. 1.6e+02; Matches 8; Conservative 2; Mismatches 7; Indels

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Search completed: May 28, 2004, 13:02:03 Job time : 13.5 secs

Sequence

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Sequence 1342, App
Sequence 1249, App
Sequence 137, Appl
Sequence 37, Appl
Sequence 63759, A
Sequence 63159, A
Sequence 6198, A
Sequence 3155, A
Sequence 12217, A
Sequence 12217, A
Sequence 20777, A
Sequence 20777, A
Sequence 20376, Sequence 12217, A
Sequence 20376, Sequence 12217, A
Sequence 20376, Appl
Sequence 20376, Sequence 1210, Appl
Sequence 210, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 1210, Appl
Sequence 1210, Appl
Sequence 1210, Appl
Sequence 215587, Sequence 1210, Appl
Sequence 1210, Appl
Sequence 215587, Sequence 10481, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6003, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
4 US-10-163-866-39

4 US-10-163-866-54

5 US-10-295-027-1249

6 US-10-295-027-1249

6 US-10-188-812-183

4 US-10-188-812-183

4 US-10-18-866-3-10

2 US-10-214-8673-10

2 US-10-425-114-63809

2 US-10-425-114-63809

2 US-10-425-114-63809

2 US-10-282-122A-65198

4 US-10-029-386-2215-5

4 US-10-186-432-703-16

5 US-10-369-493-2603

US-10-369-493-2603

US-10-369-493-2603

US-10-369-493-2603

US-10-156-4599-209396

0 US-10-156-459-209-4

0 US-10-156-459-209-4

0 US-10-156-403-4

0 US-10-164-899-215-887

0 US-10-424-599-1481-1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITITE BOSCOLORY
STATE: MASSACHUSELTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 37,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)722-7400
TELEFAX: (617)722-4214
INFORMATION FOR SEQ ID NO: 6003:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
     -10-335-977-6003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
43.5
43.5
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                                                      Sequence 6003, Ap Sequence 6004, Ap Sequence 50921, A Sequence 901, App Sequence 901, App Sequence 1159, Ap Sequence 1159, Ap Sequence 1159, Ap Sequence 23087, A Sequence 23087, A Sequence 24, App Sequence 24, 
                                                                                                                                                                         May 28, 2004, 12:57:09; Search time 34.75 Seconds (without alignments) 160.719 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1151071
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 US-10-335-977-6003
2 US-10-335-977-6004
2 US-10-284-5091
US-09-764-869-901
4 US-10-091-504-901
5 US-10-027-577-901
5 US-10-227-577-901
5 US-10-242-515-1359
5 US-10-242-515-1359
5 US-10-242-515-1359
6 US-10-238-075-91
5 US-10-238-075-91
5 US-10-259-194A-24
6 US-10-259-194A-24
7 US-10-276-774-2884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1151071 seqs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                               1 TRACRIFAFHGWNYVKVCHA 20
                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                              US-10-069-056-9
120
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136
323
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Sequence

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IITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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, APPLICANT: Rosen et al.
, TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47.5; DB 12;
Pred, No. 59;
3; Mismatches 4;
 4; Mismatches
                                                          | |::|:||:
95 CLIWSFNGWSFWEVTGLFLFYVVVCSA 121
                                 4 CRIFAFHGWN-----YVKVCHA 20
                                                                                                                                                      Sequence 50921, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 901, Application US/09764869
Patent No. US20020061521A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Bordetella pertussis
US-10-282-122A-50921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.6%;
36.4%;
                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 RIFAFHGWNYVKV---
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Best Local Similarity 36.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                          Zyskind, Judith
Wall, Daniel
     10; Conservative
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Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-764-869-901
     Matches
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5-10-335-977-6004
Sequence 6004, Application US/10335977
Sequence 6004, Application No. US20040052799A1
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DUCKEIC ACID AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 12; Length 136;
Pred. No. 22;
                                                                                                                                                                                                            Score 48; DB 12; Length 69;
Pred. No. 12;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...136
SEQUENCE DESCRIPTION: SEQ ID NO: 6004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                          ), NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...69
; SEQUENCE DESCRIPTION: SEQ ID NO: 6003:
US-10-335-977-6003
                                                                                                                                                                                                                                                                                    4 CRIFAFHGWN-----YVKVCHA 20
                                                                                                                                                                                                                                                                                                          CLIWSFNGWSFWEVTGLFLFYVVVCSA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Helicobacter pylori
          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 6004
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%;
37.0%;
                                                                                                                                                                                                                 Query Match
Best Local Similarity 37.0%;
Matches 10; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Best Local Similarity
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Gaps

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Gaps

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Sequence 149096, Application US/10424599
; Sequence 149096, Application US/10424599
; Publication No. US/2040031072A1
; Publication No. US/2040031072A1
; Publication No. US/2040031072A1
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5:223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 149096
LENGTH: 187
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 901
LENGTH: 54
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Patent No. US20020147140A1

GENERAL INFORMATION:

A PAPLICANT: Rosen et al.

TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT PAPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1359

LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_105657C.1.pep
US-10-424-599-149096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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Pred. No. 69;
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.2%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRACRIFAFHGWNYV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TSACQ--SYHSWNYV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-10-424-599-149096
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Sequence 901, Application US/10227577

Publication No. US20040005575A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PC007C2

CURRENT APPLICATION NUMBER: US/10/227,577

CURRENT FILING DATE: 2002-08-26

PRIOR FILING DATE: 2002-08-26

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR PLICATION NUMBER: 60/190,658

PRIOR PLING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-00-11

PRIOR FILING DATE: 2000-00-11

PRIOR FILING DATE: 2000-00-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 901, Application US/10091504
| Publication No. US20030059908A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| FILE REFERENCE: PC007C1
| CURRENT PILING DATE: 2002-03-07
| NUMBER OF SEQ ID NOS: 2442
| Prior Application removed - See File Wrapper or Palm
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 901
| LENGTH: 54
                              CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 901
LENGTH: 54
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                                                                                                                                                                                                                                                                                        Query Match 39.2%; Score 47; DB 9; Length 54; Best Local Similarity 53.3%; Pred. No. 13; Matches 8; Conservative 3; Mismatches 2: Timels
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.9 TSACQ--SYHSWNYV 21
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TSACO--SYHSWNYV 21
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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       FILE REFERENCE: PC007
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US-10-091-504-901
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                                                                                                                                                                                                         TYPE: PRT
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Sequence 159576, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Canou Yihua
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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US-10-44-51-1359

US-10-44-51-1359

Publication No. US20040009488A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PC005C1

CURRENT APPLICATION NUMBER: 09/764,877

PRIOR FILING DATE: 2002-09-13

PRIOR FILING DATE: 2000-00-13

PRIOR PELICATION NUMBER: 60/19,065

PRIOR FILING DATE: 2000-00-131

PRIOR PLING DATE: 2000-00-131

PRIOR PLING DATE: 2000-00-01-31

PRIOR PLING DATE: 2000-00-01-31

PRIOR PLING DATE: 2000-00-01-31

PRIOR PLING DATE: 2000-00-01-31

PRIOR PLING DATE: 2000-00-11

PRIOR PLING DATE: 2000-00-14

PRIOR PLING DATE: 2000-00-14
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Pred. No. 33;
                                                        Score 44; DB 9; Length 50;
Pred. No. 33;
3; Mismatches 2; Indels
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                                                           36.7%;
50.0%;
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50.0%;
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SEQ ID NO 1359
LENGTH: 50
                                                        Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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US-10-242-515-1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-424-599-159576
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US-10-242-515-1359
US-09-764-877-1359
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Sequence 911, Application US/10238075

Sequence 911, Application US/10238075

PUBLication No. US20330148324A1

GENERAL INFORMATION NO. US20330148324A1

TITLE OF INVENTION: FOLYMORE E.C. OF TITLE OF INVENTION: E.C. OF TITLE OF TILLION DATE: 2002-09-10

FILE REPERENCE: BLANDINE

CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT APPLICATION NUMBER: 0003145

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: PARENTING DATE: 2000-03-10

SEQ ID NO 911

LENGTH: 160
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
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Pred. No. 98;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                           Indels
                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_115116C.1.pep
                                                                                                                                                                                              Score 44; DB 12;
Pred. No. 98;
2; Mismatches 2
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23087
LENGTH: 421
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                                                                                                                                                                                                36.7%;
55.6%;
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Best Local Similarity 38.5%;
Matches 5; Conservative
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 159576
LENGTH: 159
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                                                                                                                                                                                              Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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; ORGANISM: Escherichia coli
US-10-238-075-911
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                                                                                                                                                                                                                                                                                      10 HGWNYVKVC 18
                                                                                                                                                                                                                                                                                                                               16 HGWINISIC 24
                                                                 TYPE: PRT
ORGANISM: Glycine max
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Query Match
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Matches 6; Conserv
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Sequence 2484, Application US/10276774

Sequence 2484, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT PILING DATE: 2002-11-18

CURRENT PILING DATE: 2002-11-18

PRIOR FILING DATE: 2000-04-27
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TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
                                                Gaps
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100.0%; Pred. No. 2.5e+02;
Live 0; Mismatches 0; Indels
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NAME/KEN:
LOCATION: (66)..(67)
OTHER INFORMATION: Xaa = any naturally occuring amino acid
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LOCATION: (118).
COTHEN INFORMATION: Xaa = any naturally occuring amino acid
US-10-259-194A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE OF INVENTION OF TRANSPORTED AND CHARACTERIZATION OF THE BYPERENCE 70029-WP CURRENT APPLICATION NUMBER: US/10/259,194A CURRENT APPLICATION NUMBER: US/010-09-06 PRIOR PELING DATE: 2001-09-26 PRIOR PELING DATE: 2001-09-26 PRIOR FILING DATE: 2002-04-04 PRIOR PELING DATE: 2002-04-04 PRIOR PLING DATE: 2002-04-04 PRIOR APPLICATION NUMBER: US 60/370,620 PRIOR PLING DATE: 2002-04-04 PRIOR PRIOR PLING DATE: 2002-04-04 PRIOR PRIOR PLING DATE: 2002-04-04 PRIOR PR
Best Local Similarity 38.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                           US-10-259-194A-24
. Sequence 24, Application US/10259194A
. Publication No. US20040010815A1
. GENERAL INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Gooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
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Kreps, Joel
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Provart, Nicholas
Ricke, Darrell
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239 CKLYGFSLWNYLR 251
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Best Local Similarity luv...
6, Conservative
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WESTOL 139

WESTOL 163-866-38

Sequence 38, Application US/10163866

BENERAL INFORMATION:

APPLICART: EXELIXIS, INC.

TILE OF INVENTION: SLC78 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REFRENCE: EXC2-080C

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2001-06-05

FRICH PRIOR PLILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2002-02-15

PRIOR FILING DATE: 2002-02-15

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54

SEQ ID NO 38

LENGTH: 507
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                                                                                                                                                                                                                36.7%; Score 44; DB 12; Length 507; 60.0%; Pred. No. 2.9e+02; tive 3; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUStom
SEQ ID NO 2444
LENGTH: 507
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Best Local Similarity 60.0
Matches 6; Conservative
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251 LFAYGGWNYL 260
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251 LFAYGGWNYL 260
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                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-774-2484
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CRGANISM: Homo sapiens
US-10-163-866-38
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3 10:28:19 2004
Thu Jun
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2, 2004, 15:24:48 ; Search time 652 Seconds (without alignments) 3988.623 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htgo_mus:*
em_htgo_other:*
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em vi: *
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em htg_hum: *
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em htg_other: *
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Pred. No. is the number of results predicted by chance to have a

Nueesch, J. and Rommelaere, J.
Parvovirus ns1 variants
Patent: EP 1077260-A 11 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts

REFERENCE AUTHORS TITLE JOURNAL

Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

h Length DB ID Col			d			SUMMARIES		
60 100.0 60 6 AX137746 AX137746 58.4 97.3 2019 6 AX137747 58.4 97.3 2019 6 AX137741 58.4 97.3 2019 6 AX137741 58.4 97.3 2019 6 AX137743 58.4 97.3 2019 14 PWWNPCG 58.8 94.7 4764 14 WWNPCG 58.9 94.7 4713 5007 14 AB000065 AB000065 58.9 40.8 71.3 5007 14 AB000065 58.9 84.8 71.3 5004 14 WWNRPC 58.9 87.1 5007 14 AB000065 58.0 88.0 7 5007 14 AB000065 58.0 88.0 80.9 64 AB04329 58.0 88.0 80.0 80.0 80.0 80.0 80.0 80.0	U			t t	ä	Ę	ā	
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86. 100.0 2019 6 AXI37747 AXI37747 AXI37747 B8.4 97.3 2019 6 AXI37739 AXI37739 B8.4 97.3 2019 6 AXI37739 AXI37739 B8.4 97.3 2019 6 AXI37751 AXI37751 B8.4 97.3 2019 6 AXI37754 B8.4 97.3 2019 6 AXI37754 B8.8 94.7 4761 14 MV013425 G8.8 94.7 4761 14 MV013425 G8.8 94.7 4764 14 MV013425 G8.8 94.7 5144 14 MV013426 G8.8 94.8 94.8 94.8 94.8 94.8 94.8 94.8 9	т,	09	8	09		AX137746	AXI	16 Sequenc
28.4 97.3 2019 6 AX13779 AX13773 AX13773 BS.4 97.3 2019 6 AX137743 AX137743 AX137743 BS.4 97.3 2019 6 AX137743 AX137743 AX137743 BS.4 97.3 2019 6 AX137743 AX137743 AX137743 BS.4 97.3 2019 6 AX137743 AX137743 AX137774 BS.4 97.3 2019 14 MVU34256 JU34256 MS.6 8 94.7 4764 14 MVU34256 JU34254 JU34256 MS.6 8 94.7 4764 14 MVU34256 JU34254 JU34256 MS.6 8 94.7 4764 14 MVU34256 JU34256 JU3426 J		ω,	900	2019		AX137747	AXI	7.5
58.4 97.3 2019 6 AX137743 AX137751 58.4 97.3 2019 6 AX137743 AX137751 58.4 97.3 2019 6 AX137743 AX137751 58.4 97.3 2019 6 AX137751 AX137751 58.8 97.3 2019 14 MVU14256 58.8 94.7 4764 14 MVU14255 56.8 94.7 4764 14 MVU14259 68.8 94.7 4764 14 MVU14259 68.8 94.7 4764 14 MVU14259 69.8 11.3 2007 14 AB000005 60.8 11.3 2007 14 AB000000000000000000000000000000000000		o o		2019		AX13//36 AX137730	AAL	3.5
58.4 97.3 2019 6 AX137751 AX137751 58.4 97.3 5019 1 4 PANVM2 58.8 94.7 4761 14 WNU94256 U34256 W34256 W36.8 94.7 4761 14 WNU34254 U34259 W32456 W36.8 94.7 4764 14 WU34254 U34254 W36.8 94.7 4764 14 WU34254 U34254 W36.8 94.7 4764 14 WU34254 U34258 W36.8 94.7 4773 14 HU34259 W36.8 94.7 91.3 2007 14 AB000049 AB000063				2019		AX137743	AXI	27.
58.4 97.3 5081 14 PANWARZ 56.8 94.7 4764 14 MVU34256 56.8 94.7 4764 14 MVU34256 56.8 94.7 4764 14 MVU34255 56.8 94.7 7 5144 14 MVU34255 56.8 94.7 6144 14 MVU3425 56.8 94.7 6144 14 MVU3424 56.8 7 6049 6 ARC443630 56.8 61.3 614 14 MVCCRN 56.8 7 6049 6 ARC443630 56.8 94.7 6144 900000000000000000000000000000000000		8		2019		AX137751	AX1:	775
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Parvovirus ns1 variants
Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebaforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Patent: BP 1077260-A 1 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvoviruş.
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note="unnamed protein product"
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AX137739
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                                                                                                                                RESULT 3
AX137736
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Parvovirus ns1 variants
Patent: EP 1077260-A 12 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                                                                                                                                                /mol_type="unassigned DNA"
/db_xref="taxon:10794"
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                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAC39994.1"
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ilarity 100.0%; Pred. No. 1.6e-08;
Conservative 0; Mismatches 0;
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1. .2019
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/note="parvovirus NS1 variant"
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'note="unnamed protein product"
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/codon_start=1
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                                                                                                                                                          /organism="Mice minute virus"
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Sequence 12 from Patent EP1077260.
AX137747
                                                                                        Location/Qualifiers
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Best Local S:
Matches 60
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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AX137747 LOCUS

RESULT 2

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ACCESSION VERSION

PAT 30-MAY-2001

Matches

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Parvovirus
Patent: EP
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Best Local S:
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                                                                                                                                                                                                                                             /procein id="CAC39993.1"
/db_xref="G1:14273918"
/db_xref="G1:14273918"
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RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
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                                                                                                                                                                                                                                                                                                                                                                                            PKVPTPINLLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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Parvovirus ns1 variants
Patent: EP 1077260-A 8 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                 /note="unnamed protein product"
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                                            note="Parvovirus NS1 variant"
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Sequence 8 from Patent EP1077260.
AX137743
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Matches 59; Conservative
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Minute virus of mice with two major open reading frames (genome). Voll115
Voll15. G1:60911
coat protein; genome; origin of replication; overlanning repeat.
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/db_xref="REWTREMBL:CAC39997"

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                                                                                                                         1141 ATTTGCTGTGTTTTAAACAGACCAAGGAGGCAAAAGAAATACTGTTTTATTTCATGGACCA 1200
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QTKKEVSIKTTLKELVHKRVTSPEDWMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
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RAINIHLITHTLEGDFGLYDVRGWPHT ICAMLVKRGYGSTPMSZYCAKWGKVPDWSERWAE
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TQNTGBAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Mice minute virus
Viruses; scDMA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (Dases 1 to 5081)
                                                                                             1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
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  Length 2019;
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Pred. No. 5e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Parvovirus NS1 variant"
Score 58.4; DB 6
Pred. No. 5e-08;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Mice minute virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nsl variants
1077260-A 16 21-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                        2019 bp
Sequence 16 from Patent EP1077260.
AX137751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nueesch, J. and Rommelaere, J.
                                                                                                                                                                                                                                                                                                                                    AX137751.1 GI:14273925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.3%;
Query Match
Best Local Similarity 98.3%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .2019
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CDS

FEATURES

TITLE

FEATURES

COMMENT

CDS

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VMNFYQHEWGKDGORHCHVLLGGKDESQAGKWWRQLNVYWSRNLVTACNIFPGD
VNNFYQHEWGKDGORHCHVLLGGKDESQAGKWWRQLNYWSRNLVTACNIFPGDS
RIKLREIAEDNEWYTLLTYKHKQTKXDYTKCVLFGNMIAYYFTTAKTSTSPRDGGY
FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAGETKAGRIQTKKRSVSIK
TTLKELVHKRVTSPEDWMMMQPDSYIEMMAQPGGGRNLLKWTLSICTLTLARTKTAFDL
ILERAETSKLTNFSLEDPTRTCRIFPRHOWTNYKYCHALTCVLLMRGGGKRNYTVLFRGDA
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SGGTIRIDQMCKGSKQIEPPVIMTNRENITVVRIGCERRPEHYQPIRDEMLNIHTTH
TLPGDFGLVDKNEWPNICAMLVKNGYQSTWASYCAKWGKVPDINL
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/note="unnamed protein product; Protein sequence is in
conflict with the conceptual translation; coding sequence"
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SRAGKRTRPPAYIFINQARAKKKLISSAAQOSSQTMSDGTSQPDSGNAVHSAARVERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSARSPFTTPKSTPLSQNYALTPLAŠDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
                                                                                                                                                                               The messenger RNA of this virus (colinear with the strand listed is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion.
Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C.
The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2286. 2354
/note="unnamed protein product; coding sequence"
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note="unnamed protein product; coding sequence"
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'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="unnamed protein product; coding sequence"
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                                                                                            Nucleic Acids Res. 11 (4), 999-1018 (1983)
                                                                                                                                                                                                                                                                                                                   1. .5081
/organism="Mice minute virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Drotein id="CAA24310.1"
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/db_xref="SMISS-PROT:P03137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA24311.1"
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                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                               parvovirus
                                                                                                                               83143341
                                                                                                                                                               6298737
                                                                                                                                                                                                                                                                                                                         source
                                                                                                                               MEDLINE
PUBMED
      AUTHORS
                                                                                               JOURNAL
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CDS

CDS

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The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

To as the V-strand.

The 3' and 5' termini both exhibit the potential for forming stable 'fold-back' hairpins; these sequences appear to play a role in replication [1].

The left and right halves of the genome encode two distinct, but overlapping transcriptional unite. The transcripts can be summarized [1] (1 map unit (mu) = 51 bp):

R1 (48 kb): 4.5 mu - 46 mu; 46+ mu - 95 mu R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.0 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.0 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.0 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu R3 (3.0 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
SVRYSYGKQHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGILT
NANPIGTKNDIHFSNVFNSYGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFV
CKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGGTFFWKGKLTMRAKLRANTTWNPV
YQVSAEDNGNSYMSVTKWLPTATGNWQSVPLITRPVARNTY"
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                                                                                                                                                                                                                                                                                                                                                                                                  1401 ATTTGCTGTGTTTTAAACAGACAAGAGGCAAAAGAAATACTGTTTTATTTCATGGACCA 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRL 22-MAY-1995
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The parvoviriate family cantains two groups that infect mammalian hosts: (i) defective (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-independent) parvoviruses. MVM is a member of the latter group. Both groups have been demonstrated to package both plus and minus strands (in separate particles) of the ss-DNA genome, though the minus strand is more typically packaged in the latter group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morgan,W.R. and Ward,D.C.
Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs
J. Virol. 60 (3), 1170-1174 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Original source text: Minute virus of mice (strain MVM(p)), passed
                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Astell, C.R., Thomson, M., Merchlinsky, M. and Ward, D.C. The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 5149)
Astell,C.R., Gardiner,E.M. and Tattersall,P.
DNA sequence of the lymphotropic variant of minute virus of mice
NVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
1 (bases 1 to 5149)
                                                                                                                                                                                                                                                                                                                                                       1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                            97.3%; Score 58.4; DB 14; Length 5081; 98.3%; Pred. No. 4.9e-08; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minute virus of mice, complete genome.
JO2275 MIS220 MI2521 M14704
JO2275.1 GI:332293
alternative splicing; capsid protein; complete genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5149 bp ss-DNA
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J. Virol. 57 (2), 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nonstructural protein.
                                                                                                                                                                                                                                                                                          59; Conservative
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Mice minute virus
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VERSION
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MVMPCG
                                                                                                                                                  ORIGIN
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GSYDNQTHYR FLGDGWVE I TALATRL VHLNMPKSENYCR I RVHNTTDTSVKGNMAKDD
AHEQI WTPWSLVDANAWGVWLQPSDWQY I CNTWSQLNL VSLDQE I FNVVLKTVTEQDL
GGQA I KI YNNDLTACMMVAVDSNN I LPYTPAANSMETLGFY PWKPTI AS PYRYY FCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGTTQMGVNWVSEAIRTRPA
QVGFCQPHNPPEASRAGFPARVVDADTTQGVNEANGSVRYSYGKQGHGENMABHGPA
PERVTWDETSFGGGGDTKDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
GPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQ
                                                                                                                                                                                                                                                                                                                                             GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNAVHSAA
RVERAADGPGGSGGGGGGGGGVGVSTGSYDNQTHYRPLGDGWVEITALATRLVHLNMP
KSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAA67114.1"
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/translation="MSDGTSQPDSGNAVHSAARVERAADGPGGSGGGGSGGGGVGVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDLSVTYENQEGTVEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNS
                                                                                                                                                                                                                                                                                      /trānslation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE
AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEF
                                                                                                                                                                                                                                                                                                                                                                                                                              MSQLNLVSLDQEIFNVVLKTVTEQDLGGQAIKIYNNDLTACMMVAVDSNNILPYTPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSMETLGFYPWKPT1ASPYRYYFCVDRDLSVTYENQEGTVEHNVMGTPKGMNSQFFT1
ENTQQ1TLLRTGDEFATGTYYFDTNSVKLTHTWQTNRQLGQPPLLSTFPBADTDAGTL
TAQGSRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPPAAPKVPADITQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKEANGSVRYSYGKOHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPP
LIGILITNABTGTKNDTHFSNVFNXSPOSPLARSHBSPYYGOGYWNKELDLEHKPRLH
LIGHEVOKKNAAPGOLVRLGPNLTDOYDDNOATLSRIYTYGFFWKGKLTWRAKLRAN
TTWNPVYQVSAEDNGNSYMSVTKWLPTATGNMOSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein id="AAA67110.1"
/db_xref="GI:825482"
/translation="MAPPAKRAKGKGLRDGWLVGY"
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                                                                                         join(2286. .2316,2399. .4557)
                                                                                                                                            join(2286. .2316,2399. .4557)
/gene="VP1"
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protein_id="AAA67112.1"
db_xref="G1:825483"
/translation="MVGWWGINV"
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/protein_id="AAA67113.1"
/db_xref="GI:825484"
                                                                     'note="alternative intron"
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                                                                                                                                                                                                                                   /proteIn_id="AAA67111.1"
/db_xref="GI:332294"
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/gene="VP"
/note="VP intron (alt.)"
2332. .2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF1; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2332. .2361
/gene="VP"
/note="ORF3; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="ORF2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2286. .2354
/gene="VP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2354. .2398
/gene="VP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2794. .4557
/gene="VP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="VP
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RMLNIHLTHTLPGDPGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTPINLLGSARSPFTTPKSTPLSQNYALTPLASDLEDLALBPWSTPNTPVAGTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNOLTMAGNAYSDEVIGATMILKEKSNOEVFSFVFKNENVOLNGKDIGMNSYKKELOE
DELKSLORGAETTWDGSEDMEWETTVDEMTKKOVFIFDSLVKKCLFEVLNTKNIFPGD
VNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRMLVTACNVQLFPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKLRĒJAEDNEWVTLLTYKHKQTKKDYTKCYLFGNMIAYYFLTKKKISTSPPRDGGY
FLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSYKKELQEDELKSLORGAETTWDQSEDMEWETTYDEWTKKOVFIFDSLYKKCLFEVL
NTKNI FPGDVNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLFPAERIKLRLREJAEDNEWVTLLTYKHKQTKKDYTKCVLFGNMIAVYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTKKEVSIKTTLKELVHKRVTSPEDMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGMNYVKVCHAICCVLNRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STGKSI I AQA I AQAVGNVGCYNAANVNPPFNDCTNKNL I WVEEAGNFGQQVNQFKAI C
SGQTIR I DQKGKGSKQI BPTPV I MTTNBNI TVVR I GCEERPEHTQPI RDRMLNI HL.TH
TLPGDFGLVDKNEWPMI CAWLVKNGYQSTMAS Y CAKWGKVPDWSENWAEPKVPTPINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSARSPFTTPKSTPLSQNYAL.FPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MISGSGSLNQGAKRKWAWFKVYKQLLKSVTYLFFHSVSRDAQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I LEKAETSKLTNFSLPDTRTCRI FAFHGWNYVKVCHAI CCVLNRQGGKRNTVLFHGPA
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/translation="MAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
capsid proteins, VPI (or A, 83 kd), VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2]

revises [1].
[3] sites; splice sites.
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                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:10794"
/lab_host="mouse 1 (variant A-9) cell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="nonstructural protein"
/protein_id="AAA67108.1"
/db_xref="G1:825481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="nonstructural protein"
/protein_id="AAA61109.1"
                                                                                                                                                                                                                                                             /organism="Mice minute virus"
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                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="MVM(p)"
                                                                                                                                                                                                         Location/Qualifiers
1. .5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="putative"
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/gene="VP"
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/gene="NS1"
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/gene="NS1"
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/gene="VP"
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gene="VP"
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/gene="NS1"
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/gene="NS1"
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U34255.1 GI:1464792
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Besselsen, D.G.
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Hamster parvovirus
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Matches 58; Conserv
                                                                                                                     Best Local Similarity
Matches 58; Conserv
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source
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HOU34255
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JOURNAL
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KEYWORDS
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MOU34254
LOCUS
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Mouse parvovirus 1b
Viruses; sBDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
Viruses; sBDNA viruses; Parvoviridae; Parvovirinae; Lo 4764,
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
                ö
                                                                            1401 ATTTGCTGTGTTTTAAACAGGACAAGGAAAAGAAATACTGTTTTATTTCATGGACCA 1460
                                                                                                                                                            VRL 21-AUG-1996
                                                                                                                                                                                                                                                    Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases 1 to 47cl.)

Besselsen, D.G., Pintel, D.G., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt. 5), 899-911 (1996)
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                  Gaps
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Bullding, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-AUG-1995) David G. Besselsen, Department of Veterinary Pathology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA
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94.7%; Score 56.8; DB 14; Length 4761;

Best Local Similarity 96.7%; Pred. No. 1.6e-07;

Matches 58; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                             linear
                  Indels
                                                1 ATTIGCIGIGITITIAAACAGACAAGGAGGCAAAAGAAAIGCIGITII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /specific host="Mesocricetus auratus"
/db xref="taxon:10794"
Pred. No. 4.9e-08;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mice minute virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Cutter"
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                                                                                                                                                             4761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                           Mice minute virus DNA. U34256
 Similarity 98.3%;
59; Conservative
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Besselsen, D.G.
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Besselsen, D.G.
                                                                                                                                                                                                             U34256.1 GI:1464795
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                                                                                                                                                                                                                                          Mice minute virus
Mice minute virus
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   Best Local
Matches 5
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ORGANISM
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JOURNAL
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VRL 21-AUG-1996
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1 (bases 1 to 4773)
Besselsen, D.G., Fintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
8600486
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Mouse parvovirus 1c

Mouses; asDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases) to 4764)

Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.

Molecular characterization of newly recognized rodent parvoviruses
J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                    94.7%; Score 56.8; DB 14; Length 4764;
llarity 96.7%; Pred. No. 1.6e-07;
Conservative 0; Mismatches 2; Indels 0;
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|mol_type="genomic DNA"
|specific_host="Mus musculus"
|db_xref="caxon:42842"

    .4764
    /organism="Mouse parvovirus lb"
/mol_type="genomic DNA"
/specific host="Mus musculus"
/db_xref="taxon:42841"

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115. .2280
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QVNQFKAICSGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVKIGCSERPEHTQPIRD
RMINHLTHTLEGDFGLVDKNEWPMICAMLVKNGYQSTWASYCAKWGKVPDWTENWAE
PKYPTPINSLGSARSPFTPKSTPLSQYPALTPLASDLEDLALEPWSTPNTFVAGTAE
TQNTGEAGSKACQDGLSPTWSETEBELRACFGAEPLKKDFSEPLNLD"
JOIN (2290. .2320, 2403. .4561)
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nnykkeloedelkslorgaettwdosedmewestvdemtkkovpiydslykkclfevl
stkniapadvtwfvohewgkdogmhchvliggkdfsoaggkwwrrolnywsrwlvta
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Viruses; seDNA viruses; Parvoviridae; Parvovirus.
Ball.Goodrich, L.J. and Johnson, E.
Molecular characterization of a newly recognized mouse parvovirus
V. Virol. 68 (10), 6476-6486 (1994)
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                                                        Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department
Veterinary Pathology, University of Missouri-Columbia,
Veterinary Medicine Building, Columbia, MO 65211, USA
Location/Qualifiers
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/db_xref="G1:525326"
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/organism="Mouse parvovirus 1"
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/gene="NS1"
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2 (bases 1 to 4773)
Besselsen, D.G.
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Ball-Goodrich, L.J.
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KSENYCKUR VHINTNDTRTAGNANDAHEQIWTPUSLIDSNANGVERPEN MANTHER KSENYCKUR VHINTNDTRTAGNANDAHEQIWTPUSLIDSNANGVERPEN MASHVILLASLOGELFUVVI KTYTEQNTGAEAVKI YNNDLTASNAVALDSNN I LPYTPAT MORTIGLEY PWKETPMES BYYTY FOOTSSI VYTYDOKSI STOTYBANASGLSOGFTIE NTORIGILR TGDERFATTEY FETER I KLSHTWOSNRQLIGOPPO I TDLEPTADNENATLY TRGDRSGI TQI SGSNDVTEATR VRPAQVGFCQPHDNPET SRAGPFKVPVVPANVTQGN EHDANOSLIRYTYDKOHGOMGSNNSKERFTWDA I SYDSGRANDRCFINATPFTSPPAL NNI LINSDPIGNKTA I HYDVYDVPNSYGPLIAFPPPPPAL SYDSGRANDRCFINATPFTSPPAL OAPFVCKNNABGOLL VRALAPNITDQYDPNSSTLSR I VTYGTFFWKELDLEHKPRLHA QAPFVCKNNABGOLL VRALAPNITDQYDPNSSTLSR I VTYGTFFWKELDLEHKPRLHA TWNPVYQVSAQYQNENEYMSI HKWLPTATGNMQSI PLLSR PVARNITY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56.8; DB 14;
Pred. No. 1.6e-07;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .5085
/organism="Mice minute virus"
/mol_type="genomic DNA"
/isolate="lymphotropic variant"
/db_xref="taxon:10794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="G1:82547?"
|Oin(2290. .2320,2403. .4561)
|gene="VP1"
|codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5085 bp ss-DNA
                                                                                                        protein"
                                                                                                 /product="capsid protein'
/protein_id="AAA61406.1"
/db_xref="G1:525327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prototype strain
J. Virol. 570, 656-669 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="NS1"
/note="putative"
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mRNA

CDS

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à
                          STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEBAGNFGQQVNQFKAIC
GOOTIRIDOKGKGSKQIEPPPVIMTINBNITVVRIGCERRPBHTQPIADRALAIHLTH
TLPGDFGLVDKNEWPMICAMLVKNGYGSTMASYCAKMGKVPDWSENWAEPKVPTPINS
LGSARSPFTTPKSPFSLGNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGG
KACQDGQLSPTWSEIEBDLRACFGAEPLKRDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVNQFKAICSGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRD
RMLNIHLTHTLPGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
PKVPTPINSLGSARSPFTTPKSTFLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MAGNAYSDEVLGTTNWLKEKSNOEVFSFVFKTEDVQLNGKDIGW
YNYKKELQDEDELKSLQRGAETTWDQSEDNEWESTYDDEWTKKQVPIYDSLYKKCLEBVU
SNYKKIJAPDPDELKSLQRGAETTWDQSEDNEWESTSQAQGKWWRRQLNVYWSRWLVTA
STRVIAPADYTWFVQHEWGRQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
CNVQLYPADER KILEBLAEDSEWYTLLYKHKQTKKDYTKKOYLFGNMIAYYFLTKKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGV
DREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPP
LNGILTNANPIGTKNDIHFSNVFNSYGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLH
I LEKAETSKLTNFSLPDTRTCKI FAFHGWNYVKVCHA I CCVLNROGGKRNTVLFHGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARTKTAFDLILEKAETSKLTNFSLPDTRTCKIFAFHGWNYVKVCHAICCVLMRQGGKR
NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYDQYIKSGKNPYLYFSAADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLATDSEP
GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTWSDGTSQPDGGNAVHSAA
RVERAADGPGGSGGGGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSENYCRIRVHNTTDTSVKGNMAKDDAHEQIMTPWSLVDANAWGVWLQPSDWQYICNT
MSQLNLVSLDQEIFNVVLKTVTEQDSGGQAIKIYNNDLTACMMVAVDSNNILPYTPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTKKEVSIKTTLKELVHKRVTSPEDWMMMQPDSYIEMMAQPGGENLLKNTLEICTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENTQQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITAPFVCKONAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRAN
ITWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSMETLGFYPWKPTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rontgeagskacodgolsptwseleedlracfgaeplkrdfseplnld"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="major transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription start site"
                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="nonstructural_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2282. .2377

gene="VP"

fnote="alternative intron"

join(2287. .2317,2400. .4558)

gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Join(2287, .2317,2400, .4558)
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _note="alternative intron"
                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="AAA69567.1"
db_xref="GI:332291"
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'db xref="GI:332290"
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/gene="VP1"
/note="ORF1; putative"
/codon_start=1
                                                                                                                                                                                                                                                              'product="NS-1 mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="VP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="VP"
                                                                                                                                                                                           201. .>2280
/gene="NS1"
                                                                                                                                                                                                                                                                                                                       /gene="NS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cou3. .2281
'gene="VP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="VP
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gene

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exon

exon

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gene

CDS

CDS

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coat protein; genome; origin of replication; overlapping genes; terminal repeat; unidentified reading frame.

Mice minute virus
Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (Dases 1 to 5087)
Sahli,R., McMaster,G.K. and Hirt,B.

DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDD
AHEQIWTPWSLVDANAWGVWLQPSDWQYICNTWSQLNLVSLDQEIFNVVLKTVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGPA
RERTYWDETHYRGSGRDTRDGFLQSAPLVVPPPLANGILTNBANFIGTKNDIHESNVFNSY
GPLTAFSHFSPYYGGGQINMCRIDLEHKPRIHITAPFVCKNNAPGQMIVRLGSHXLTDG
YDPNGATLSRIVTYGTFFWKGKLITMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Mouse parvovirus minute virus immunosuppressive variant genome ( =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:32292"
/translation="MSDGTSQPDGGNAVHSAARVERAADGPGGSGGGGSGGGGVGVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1402 ATTTGCTGTGTTCTAAACAGACAAGAGGCAAAAGAAATACTGTTTTATTTCACGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATTIGCTGTTTTAAACAGACAAGAGGAGCAAAAGAAATGCTGTTTTATTTCATGGACCA
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0
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/protein id="AAA65568.1"
/branslation="MAPPARRAKRGKGLRDGWLVGY"
/translation="MAPPARRAKRGKGLRDGWLVGY"
/gene="VP1"
/unmber=2
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/protein id="AAA69570.1"
/bxref="G1:825479"
/translation="WYGWWGINV"
2355. .2399
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'db_xref="GI:825480"
                                                                                                                                                                                                                 'note="alternative intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  id="AAA69572.1"
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                                                                                                                                                                                                                                  2333. .2362
/gene="VP1"
/note="ORF3; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VP1"
/note="ORF2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGNMOSVPLITRPVARNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                          codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/protein_id="A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2400. .>4558
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2795. .4558
/gene="VP2"
2795. .4558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2795. .4558
/gene="VP2"
                                                                                                                                                                   2318. .2399
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'number=2
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                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
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Matches
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PAMVMI
                                                                                                  exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
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TKNDI HFSNVFNSYGPLTAFSHPSPVY PQGQI WDKELDLEHKPRLHI TAPFVCKNNAP
GQML VRLGPNLTDQYDPNGATLSR I VTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVE
DNGNSYMSVTKWLPTATGNMQSVPL I TRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRDĽSVTYENQEGTI EHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTN
PVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRP
AQVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTIASPYRYYFCVDRDLSVTYENOEGTIEHNVMGTPKGMNSOFFTIENTQOITLLRTG
DEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQM
EVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPPAAPKVPADVTQGVDREANGSVRYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNS
YGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDGGNGVHSAARVERAADGPGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3GGGSGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTWSQLNLVSLDQE
FNVVLKTVTEQDSGGQAIKIYNNDLTACMMYAVDSNNILPYTPAANSMETLGFYPWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKOHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="TMSDGTSQPDGGNGVHSAARVERAADGPGGSGGGGSGGGGGGGG
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DAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQD
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autonomous parvovirus, minute virus of mice Nucleic Acids Res. 13 (10), 3617-3633 (1985) 85242059
385542.
For the fibroblast-specific strain (MVMp) sequence see <PAMVM2>.
The genomes of MVMp and MVMmi (immunosuppressive variant) have more than 96% of their sequence in common.
Data kindly reviewed (18-JUL-1986) by G. McMaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="VPPGYKYLGPGNSLDQGEPTNPSDAAKEHDEAYDQYIKSGKNP"
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'note="polyadenylation signal"
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xref="SWISS-PROT:P07302"
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92.0%; Score 55.2; DB 14; Length 5087; 95.0%; Pred. No. 4.9e-07;

Query Match Best Local Similarity

Search completed: June 2, 2004, 18:58:36 Job time: 652 secs

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not include start and stop codon"
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/*tag= b
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variant (T394A) DNA shown in AAD02803
ALIGNMENTS
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/product= "Parvovirus
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P-PSDB; AAY72707.
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                                 The present sequence is a parvovirus non-structure protein (NSI) variant (T394A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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               Disclosure, Page 21-22, 41pp; English.
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Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
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(first entry)
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                                                                                                             60; Conservative
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                                                      Query Match
Best Local Similarity
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                        AAD02801;
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AAD0280 RESULT

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The present sequence is a wild type DNA encoding parvovirus non-
structure protein 1 (NS1). The present invention relates to the variants
of the parvovirus non-structure protein (NS1) having a shifted
equilibrium between the DNA replication and transcription activities, and
the cytotoxicity activity. These variants are useful as toxins for
treating tumoural diseases. The variant DNAs are useful as vectors for
gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                 NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 97.3%; Score 58.4; DB 5; Length 2019; 1. Similarity 98.3%; Pred. No. 1.7e-09; 59; Conservative 0; Mismatches 1: Indela n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2019 BP; 698 A; 389 C; 452 G; 480 T; 0 U; 0 Other;
                                                                           Parvovirus non-structure protein 1 (NS1) wild-type DNA
                                                                                                                                                                                                                                                                     /product= "Parvovirus NS1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                            Location/Qualifiers
1. .2019
/*tag= a
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                     (revised)
(first entry)
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P-PSDB; AAY72702.
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Best Local Similarity
Matches 59; Conserv
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                     06-AUG-2003
31-MAY-2001
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31-MAY-2001
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                                                                                                                                                                          Parvovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
AAD02799
                                                                                                                                                                                                                Key
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1141 ATTTGCTGTGTTTTAAACAGACAAGGCAAAAGAAATACTGTTTTATTTCATGGACCA 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                       NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
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/product= "NS1 variant (T463A) protein"
replace(1387, A)
/*tag= b
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1. .2019
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                                                                                                                   AAD02805 standard; DNA; 2019
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(first entry)
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                               Parvovirus.
Synthetic.
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Gaps ö 9

Parvovirus Synthetic.

AAD02797 standard; DNA; 2019 BP

RESULT 5
AAD02797
ID AAD0
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AC AAD0

Matches

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AAD02797

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Gaps

mutation

Key

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This viral DNA is isolated from a non- attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEM5Z. The host cells to be transfected ar selected from Norden Liaboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
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                                                                   Attenuated CPV strains contg. up to 4 mutation (8) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.8; DB 2;
Pred. No. 0.00027;
0; Mismatches 7;
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                                                                                                                                                                               Claim 1; Page 21-24; 42pp; English.
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Best Local Similarity 87.0%;
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2019 BP; 698 A; 389 C; 453 G; 479 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                "NS1 variant (S283A) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-attenuated canine parvovirus CPV-39 passage 5 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58.4; DB 5;
Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parrish CR, Gruenberg A, Carmichael LE;
                                                                                                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 11-14; 41pp; English.
                                                        /*tag= a /product= "NS1 v replace(847, A) /*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-00336345.
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                                                                                                                                                                                                                                                                                              99EP-00115161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-212717/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canine parvovirus
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                                                                                                                                                                                    EP1077260-A1
                                                                                                                                                                                                                                                                                              13-AUG-1999;
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                                                                                                                                                                                                                                             21-FEB-2001
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AAT15311

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15-MAY-1996;
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21-MAY-1998
                                                                                                                                      Parrish CR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation
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feline
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Matches
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                                                                       This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEM5Z. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= "base 4307 is A in virulent CPV-39 (G in passage
65 attenuated virus)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in passage
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
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feline panleukopenia virus; mink enteritis virus; infection; ds
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                                                                                                                                                                                                                                                                         Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            71.3%; Score 42.8; DB 2; Length 5049; 87.0%; Pred. No. 0.00027; Live 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    £
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65 attenuated virus)"
4477
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/note= "base 4889 is C in virulent CPV-39
65 attenuated virus)"
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attenuated virus)"
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/note= "NS1/NS2 coding region"
2286. .4541
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'note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                         Claim 2; Page 24-27; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                canine A72 cells
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                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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AATSB3
X & X & S & S & S & S & S & S & S
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Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Attendated viruses are obtained by serial passage of the virulent CPV type 2b isolate 39 in NLFK feline kidney host cells. They have one or more of the sequence relaterations indicated in the sequence relative to the sequence relative to a claimed virus from the 65th passage) wild-type CPV-2b (see AAT88320). A claimed virus from the 65th passage (deposited as ATCC VR 2528) contains all 6 mutations. The DNA from attenuated CPV strains (see also AAT88324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protect against CPV disease, or more generally in cats and minks to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parvovirus; CPV; attenuation; vB1440; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 71.3%; Score 42.8; DB 2; Length 5049; Local Similarity 87.0%; Pred. No. 0.00027; les 47; Conservative 0; Mismatches 7; Indels 0.
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"base 59 is G in CPV-39 (passage 5)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "VP1/VP2 coding region"
4745
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                                                                                                                                           Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine parvovirus; vBI440 (ATCC VR 2489)
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"base 97 is
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note= "NS1/NS2
                                                                     (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT88324 standard; DNA; 5049
96US-00647655.
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4541
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                         WPI; 1998-008583/01
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This DNA sequence comprises an attenuated virus genome derived by serial passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate (C 39 in NLFK feline kidney host cells. The attenuated virus is designated the NELATOR 2489). It contains 4 mutations relative to the sequence (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations at micleotide 59 introduces an A into a G-C rich region within the tip of the hairpin, disrupting the base pairing in one of the 2 small internal companient to the mismatched bubble (file)-flop) sequence within the top adjacent to the mismatched bubble (file)-flop) sequence within the CC adjacent to the mismatched bubble (file)-flop) sequence within the cut an attenuated CPV strains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in the time, an be transfected into cells to generate master stocks of the against CPV disease, or more generally in cats and minks to protect against the currently prevalent cats and minks to protect protect against the currently prevalent cats and minks in the variant contect against the currently prevalent term immune response.

CC (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                       Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1422 TGTGTTTTAAATAGACAAGGGGTAAAAGAAATACAGTTCTTTTCATGGACCA 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine parvovirus; CPV; attenuation; vB1440; vaccine; dog;
feline panleukopenia virus; mink enteritis virus; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TGTGTTTTAAACAGACGAGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.3%; Score 42.8; DB 2; Length 5049; 87.0%; Pred. No. 0.00027; tive 0; Mismatches 7; Indels 0;
         "base 4745 is T in CPV-39 (passage 5)"
                                                                /note= "base 4881 is C in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canine parvovirus 39 passage #5 (wild-type).
                                                                                                                                                                                                                                                                                        Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine parvovirus; type 2b isolate 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; Page 34-37; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT88320 standard; DNA; 5049 BP
                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                  96US-00647655.
                                                                                                                                                                               97WO-US007584
                                                                                                                                                                                                                                                                                        Parrish CR, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Conservative
ø
/*tag=
/note=
                                                     /*tag=
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                                                                                                                                                                                                                                                                                                                            WPI; 1998-008583/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-0CT-2003
21-MAY-1998
                                                                                                                                                                               36-MAY-1997;
                                                                                                         WO9742972-A1
                                                                                                                                               20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT88320;
                                    mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT88320
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This DNA sequence comprises the genome of virulent canine parvovirus type 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline 2b (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline 2c (ArCC VR 2489) (see AAT88324) from the 60th passage, and a claimed virus (ArCC VR 2489) (see AAT88324) from the 60th passage, and a claimed virus (see AAT88321) derived from the 65th passage (ATCC 2528). These cespectively contain 4 and 6 mutations in comparison to the virulent 5th passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The CPV disease, or more generate master stocks of the virus. The CPV disease, or more generally in cats and minks to protect against currently prevalent cPV-2b vype (and all extant strains of types 2 and 2a), and provide a long term immune response. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                          Canine parvovirus DNA carrying specific attenuating mutation(8) - used as vaccines for protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1422 İGİÇİTİTAAATAGACAAĞGTĞTĞTAAAGAAATACAĞTTCİTİTİTĞĞAÇĞA 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence from the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein envelope; immunogen; vaccine; antigen; epitope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 11.3%; Score 42.8; DB 2; Local Similarity 87.0%; Pred. No. 0.00027; nes 47; Conservative 0; Mismatches 7;
                                                                               /*tag= b
/note= "VP1/VP2 coding region"
             273. .2279
/*tag= a
/note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine parvovirus; NADL-2 virulent strain.
                                                                                                                                                                                                                                                                                    Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 37-40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .2073
cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN40252 standard; DNA; 3524 BP.
                                                                                                                                                                                                                                                      (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                         97WO-US007584.
                                                                                                                                                                                                                        96US-00647655.
                                                                                                                                                                                                                                                                                     Carmichael LE,
                                                              .4541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                  2286.
                                                                                                                                                                                                                                                                                                                   WPI; 1998-008583/01.
                                                                                                                                                                                                                                                                                                                                                                                virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2003
12-JAN-1992
                                                                                                                                                                                          06-MAY-1997;
                                                                                                                                                                                                                        L5-MAY-1996;
                                                                                                                             WO9742972-A1
                                                                                                                                                                                                                                                                                       Parrish CR,
                                                                                                                                                           20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parvovirus.
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Matches
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   Key
                                                                  CDS
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The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymuclectides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable trains as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                   New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 ATTTGCAGAGTGTTCAATAAACAGGAGACAGAAAAAATGTTGGATTAATCCAT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                       Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 28579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 1005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1005 BP; 297 A; 244 C; 223 G; 241 T; 0 U; 0 Other;
                       Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 28579; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
   Dubell AT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28.4; DB 9;
Pred. No. 11;
0; Mismatches 16;
Adam LJ, Dubell Arril, Creelman RA,
                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 446; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                       Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL25702 standard; DNA; 2675 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
   Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.4
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster,
                     Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                              2003-248221/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                              WPI; 2003-248221/
P-PSDB; ADD30418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
 Ratcliffe O,
Pilgrim ML,
                                                                                                                                                                                                or apomixis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC,
                                             Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL25702;
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     SXCCCCCCCCCXXXXIIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ទ
                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inventors claim an immunologically active polypeptide for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.4; DB 1; Length 3524;
Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 3524 BP; 1400 A; 719 C; 648 G; 757 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1157 İGAAACAGACAAGAGAAAAAGAAAİACAAİİCİAİTİCAİG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Table II, Page 33-49; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
   '*tag= a ·
'note= "see AAP40306"
2107. .3522
                                                          /*tag= b
/note= "see AAP40675"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEND-) MENDEL BIOTECHNOLOGY INC.
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11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2002; 2002WO-US025805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001; 2001US-0310847P
                                                                                                                                                                                            84WO-US000063
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86.0%;
                                                                                                                                                                                                                               83US-00459203
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                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAP40306, AAP40675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1984-201354/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN
                                                                                                                                                                                            19-JAN-1984;
                                                                                                                                                                                                                                 19-JAN-1983;
                                                                                                                                                                                                                                                     06-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2004
                                                                                                                   WO8402847-A
                                                                                                                                                     02-AUG-1984
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABP72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Sequence 2675 BP; 728 A; 558 C; 654 G; 735 T; 0 U; 0 Other;

ö Gaps ö DB 4; Length 2675; 13; Indels 0; Mismatches Score 28.2; I Pred. No. 15; 47.0%; Query Match
Best Local Similarity 73.5
Matches 36; Conservative

57 9 TGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA g

8

ABL25700 standard; DNA; 3049 RESULT 15 ABL25700 ID ABL2

ABL25700;

(first entry) 26-MAR-2002 Drosophila melanogaster genomic polynucleotide SEQ ID NO 28573.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001

23-MAR-2001; 2001WO-US009231

23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150

(PEKE) PE CORP NY

Myers EW Li PWD, Venter JC, Adams M,

WPI; 2001-656860/75

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions

Claim 1; SEQ ID NO 28573; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 3049 BP; 767 A; 685 C; 765 G; 832 T; 0 U; 0 Other;

Query Match

47.0%; Score 28.2; DB 4; Length 3049;

ö Gaps . 0 741 TATTITIAAAAGCCCAGTAGGTACAAGGAATGATTITCTATCTATGGA 789 57 9 TGTTTTAAACAGAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA 13; Indels Pred. No. 16; 0; Mismatches 73.5%; 36; Conservative Best Local Similarity Matches 36; Conserv g ò

2, 2004, 19:08:33 Search completed: June Job time : 148.25 secs RH03914.5 603536587

Scoring table:

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Minimum 1 Maximum 1

Database

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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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Fax: 301-838-0208
Email: ekirknes@tigr.org
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Copyright (c) 1993 - 2004 Compugen Ltd.
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GSS 24-SEP-2003

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Result Š. 4.0.4.0

2230

GSS 04-OCT-2000

Class: shotgun.

FEATURES

ORIGIN

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb/2 (gil #4732114|gbh/R129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. ooli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                        Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 646)

Unn,D., Aoyagi,W., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niderhausern,A. and Wright,D.,Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                         AZ445628 646 bp DNA linear GSS 04-OCT-200
1M0241106R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0241106 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""Vector: PWD42nv; Purified genomic DNA from M.
musculus G79BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTIGCTGTGTTTTAAACAGACGAAGGCAAAAGAAATGCTGTTTTATTTCAT
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47.3%; Score 28.4; DB 28; Length 646;
Best Local Similarity 70.4%; Pred. No. 2.6e+02;
Matches 38; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
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/mol type="genomic DNA"
/strain="C57BL/63"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ101675
HS 3014 Al_C10 T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3014 Col=19 Row=E, genomic survey
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and
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48.7%; Score 29.2; DB 28; Length 414;
Best Local Similarity 67.8%; Pred. No. 1.7e+02;
Matches 40; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                            Length 661;
                                                                                                                                                                                                                                                                                                                                                                                               3 TIGCIGIGITITIAAACAGACAAGGAGGCAAAAGAAAIGCIGITITAIT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-388
Fax: (206) 616-388
Fax: (206) 616-388
                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                            Score 30.4; DB 29;
Pred. No. 68;
0; Mismatches 11;
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/db_xref="taxon:9606"
/clone="Plate=3014 Col=19 Row=E"
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Location/Qualifiers
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Location/Qualifiers
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AQ101675.1 GI:3472704
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Best Local Similarity 77.1%;
Matches 37; Conservative (
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Class: BAC er
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0449764

MEDLINE PUBMED

FEATURES

ORIGIN

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JOURNAL

TITLE

Hood, L.

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

AQ101675/c DEFINITION

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PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                Rubin, G.M.
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BU397481/c
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                                CD731301 509 bp mRNA linear EST 26-JUN-2003 4040794 1GAL - Chicken Intestinal Lymphocyte Gallus gallus cDNA clone 1GAL_53G04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hlilleho@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '' -trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 12
Plate: 53 row: G column: 04
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Habasianinae, Gallus.

1 (bases 1 to 509)

Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van Tassel, C. and Han, J.Y.

Chicken intestinal lymphocyte EST database as a resource for the analysis of mucosal immune function
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clome_lib="1GAL - Chicken Intestinal Lymphocyte" | /orde="forgan: Intestina; Vector: pGWV-SPORT6; Site_1: Sal1; Site_2: Not1; Normalized library from chicken gut infected with coccidia duodenum and middle gut."
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47.0%; Score 28.2; DB 14; Length 509;
Best Local Similarity 73.5%; Pred. No. 3.1e+02;
Matches 36; Conservative 0; Mismatches 13; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA 57
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg.1043, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /moi_type="mRNA"
/strain="white leghorn SC"
/db_xref="taxon:9031"
/clone="1GAL_53G04"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Gallus gallus"
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Seg primer: ATTTAGGTGACACTATAG
High quality sequence stop: 509.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Lymphocyte"
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/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Gut"
                                                                                                                          CD731301.1 GI:32282150
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BIS90311.1 GI:15481733
                                                                                                                                                                  Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 3015045103
                                                                                                  CD731301
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BIS90311
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RESULT 4
CD731301/c
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Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases I to 530
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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603536587F1 CSEQCHN58 Gallus gallus cDNA clone ChEST499m21 5', mRNA
                          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.

1 (base 1 to 536)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Frise, E., Gearlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guorin, H., Harris, N., Li, P., Liao, G., Pholana, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Pholanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anote="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Fiero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003603: arm:3R [972216,1267129]
estimated-cyto:82F1-83A4: 08/16/2001
Plate: RH.39 row: B column: 2
High quality sequence stop: 440.
Location/Qualifiers
i. 536
/organism=Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male and female"
/dev_stage="Adult"
/lab_host="DHS-alpha TonA"
/clone_lib="RH Drosophila melanogaster normalized Head
pPlc-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                             BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RH03914"
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BU397481.1 GI:25766537
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Stapleton, M.
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Gaps

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EST 25-APR-2001

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Eutheria; Cetartiodactyla; Ruminantia, Pecora; Bovoidea, Bovidae, Bovinae; Bos.

Bovidae, Bovinae; Bos.

(CB 1 (bases 1 to 446)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Reele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from day 20 and day 40
embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATTTGCTGTGTTTTAAACAGACAGAGGGAAAAGAAATGCTGTTTTATTTCATGGACCA
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/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                       Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 446;
                                                                                                                                                                                                                                                                                                                                                                       BE722343
190538 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                      Indels
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                                                                                                                                47.0%; Score 28.2; DB 29;
68.4%; Pred. No. 3e+02;
Live 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch
1 Similarity 66.7%; Pred. No. 3.7e+02;
40; Conservative 0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="mRNA"
/db xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACACCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 102 row: G column: 21
Seg primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
                                                                                                                                                                              39; Conservative
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Bos taurus
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Matches 40; Conserv
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Best Local Similarity
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//dev stage="adult"
//dev stage="adult"
//dev stage="buloB"
//clone_lib="CSEQCHNSB"
//clone_lib="CSEQCHNSB"
//clone_lib="CSEQCHNSB"
//clone_lib="CSEQCHNSB"
//site_l: EcoRI; Site_2: Not1; This normalized
KS(+): Site_l: EcoRI; Site_2: Not1; This normalized
Ilbrary was constructed from 1 million independent clones.
CDNA synthesis was initiated using an oligo(df) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI; size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., pNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tigr-gss-dog-17000322038797 Dog Library Canis familiaris genomic, genomic survey sequence.
CE021004
GE021004.1 GI:35033318
GSS.
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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Canis familiaris
Canis familiaris
Canis familiaris
Canis familiaris
Bukaryota: Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 595)
1 (karness, E.F., Baffna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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47.0%; Score 28.2; DB 13; Length 538;
Best Local Similarity 73.5%; Pred. No. 3.1e+02;
Matches 36; Conservative 0; Mismatches 13; Indels 0;
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/strain="Standard Poodle"
/db_xref="taxon:9615"
                                                                                                                                                                      /mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST499m21"
                                                                                                                                                   /organism="Gallus gallus"
                                      Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@unist.ac.uk.
Location/Qualifiers
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Coordinated Laboratory for Computational Genomics
                         Contact: Soares, MB
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les 35; Conserv
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                                       BQ427038 518 bp mRNA linear EST 01-SEP-2002 CgHem 027-A-16 C. gigas Hemocytes Lambda Zap Express Library Crassostrea gigas cDNA, mRNA sequence.
                                                                                                                                                                                                                Eukaryotta; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida; Ostreoidea; Ostreoidea; Crassostrea.

1 (bases 1 to 518)
1 (bases 1 to 518)
2 (doeguen, Y., Cadoret, J.P., Flament, D., Barreau-Roumiguiere, C., Girardot, A.L., Garnier, J.P., Hoareau, A., Bachere, E. and Escoubas, J.M. Immune gene discovery by expressed sequence tags generated from hemocytes of bacteria-challenged oyster, Crassostrea gigas Gene 303, 139-145 (2003)
Defenses et Resistances chez les Invertebres Marins
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DRIM, CNRS-IFREMER, CC80, 2 Place E. Bataillon, Montpellier 34095,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Normalization and subtraction: two approaches to facilitate gene
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UI-R-CA1-bil-c-02-0-UI.sl UI-R-CA1 Rattus norvegicus cDNA clone
UI-R-CA1-bil-c-02-0-UI 3', mRNA sequence.
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66.7%; Pred. No. 3.6e+02;
ive 0; Mismatches 20; Indels
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Seq primer: T3 primer: aattaaccctcactaaaggg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Crassostrea gigas"
                                                                                                                                                                            Crassostrea gigas (Pacific oyster)
Crassostrea gigas
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/db_xref="taxon:29159"
/cell_type="hemocytes"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (0) 467144625
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/clone="UI-R-CA1-bil-c-02-0-UI"
/lab_host="UHIOB (Life Technologies)"
/lab_host="UHIOB (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco R1; The UI-R-CA1
library is a subtracted library derived from the following
tissues: thalamus, cereballum, hypochalamus, medalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA710811 402 bp mRNA linear EST 24-DEC-1997 vt93d02.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1178691 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest-eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ilarity 74.5%; Pred. No. 4.6e+02;
Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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TAG_LIB=UI-R-CA1
TAG_SEQ-GATGC"
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The WashU-HHMI Mouse EST Project
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FEATURES

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MGI:506832
MGI:697405
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AA509795/c
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JOURNAL
COMMENT
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Matches
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KEYWORDS
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Mus musculus
Mus musculus
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Merazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra, M., Hallier, L., Allen, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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ua34d03.rl Soares mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1348613 5', mRNA sequence.
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The WashU-HMIM Mouse EST Project
Unpublished (1996)
Contact: Marra M Mouse EST Project
Contact: Marra M Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Eax: 314 286 1810
Email: mousesestGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
MGI:636539
Seq primer: -20mi3 rev2 Erf from Amersham
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  Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4.38+02;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                               'organism="Mus musculus"
                                                                                                                                                                                     High quality sequence stop: 395.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:1178691"
                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity 69.1%;
Matches 38; Conservative (
                                                                                                                                                                                                                          :405
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ORGANISM
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JOURNAL
COMMENT
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AA981917/c
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AUTHORS
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KEYWORDS
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ORIGIN

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 468)
Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Marra, M., Hillier, L., Allen, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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468 bp mRNA linear EST 08-JUL-1997 vg29a09.r1 Soares mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:862744 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             daptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="mammary gland"
/dev stage="4 weeks"
/lab_host="DH10B"
/clone lib="Soares mammary gland NDMMG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(pharmacia) with a modified polylinker; Site 1: Not I:
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Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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High quality sequence stop: 381.
Location/Qualifiers
-28m13 rev2 ET from Amersham
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/mol_type="mRNA"
                                                                                                             /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
        Seg primer: -28ml3 revz El LLOWN
High quality sequence stop: 448
Location/Qualifiers
                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:1348613"
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Mus musculus
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COMMENT
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Maize ESTs from various cDNA libraries sequenced at Stanford
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Pred. No. 4.2e+02;
0; Mismatches 17; Indels (
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                 type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: walbot@stanford.edu
Plate: 660053 row: A column: 04.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Walbot V
Department of Biological Sciences
             db_xref="taxon:10090"
                         /clone="IMAGE:862744"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Ohio43"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AW499334
AW499334.1 GI:7137911
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Unpublished (1999)
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Best Local Similarity 69.1
Matches 38; Conservative
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SOURCE
ORGANISM
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AUTHORS
TITLE
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46.3%; Score 27.8; DB 10; Length 541;

Query Match

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/tissue_type="nucellar, embryo, and endosperm"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_hosge="10-14 days post-pollination"
/lab_hosge="10-14 days post-pollination"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoR1;
Site_2: Xhol; Kernel endosperm cDNA library from Schmidt
lab"
                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                            71 TAGCTGTAATCTATACAGACAAAAATATTGTAGAAGTGTTGTTCATTTCAATTTCAAGGA 17
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Stanford University
Scalifornia Ave, Palo Alto, CA 94304, US
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbocestenford.edu
Plate: 605007 row: B column: 08.
Pred. No. 4.1e+02;
                                  0; Mismatches
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/mol type="mRNA"
/cultivar="Ohio43"
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Job time : 1505.5 secs
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            L Similarity 69.1%;
38; Conservative
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AI665130
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Unpublished (1999)
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Matches 38; Conser
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VERSION
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TITLE
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Sequence 3 Sequence 3 Sequence 3

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Sequence 7, Appli Sequence 131, App Sequence 3, Appli

US-09-673-395A-19 US-09-673-395A-531 US-09-731-166-7 US-09-325-932A-131 US-09-245-041-3

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ORGANISM: Parvovirus
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TYPE: nucleic acid
STRANDEDNESS: both
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Sequence 2860, Ap
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Sequence 1581, Ap
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Sequence 55, Appl
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Sequence 1178, Appl
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Sequence 1178, Appl
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Sequence 1581, Ap
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Sequence 1581, Ap
Sequence 2551, Ap
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Sequence 1, Ap
Sequence 54, A
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. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-998-416-55

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1422 IGIGITITIAAATAGACAGGGGGAAAAGAAATACAGTTCTTTTCATGGACCA 1475
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Parrish, Colin R. APPLICANT: Parrish, Colin R. APPLICANT: Caucherg, Allen APPLICANT: Carmichael, Leland E. TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESSE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: NY ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS CORPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS CORPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS CORPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPUTER: IBM PC COMPATION ATTORNS CORPU
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Sequence 1, Application US/08647655
Patent No. 5885585
GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           Sequence 2, Application US/08336345
Patent No. 5814510
GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: both
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Matches 47; Conservative
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ORIGINAL SOURCE:
ORGANISM: Parvovirus
US-08-336-345-2
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STREET: 1155
CITY: New York
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Sequence 2, Application US/08647655

Patent No. 588585

GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Gramichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
INUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
STATE: New York
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CAPPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,655
FILING DATE: On Even Date Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 7937-008
TELEPHONE: (212) 790-900
TELEPHONE: (212) 790-900
TELEPHONE: (212) 790-900
TELEPHONE: (212) 780-900
TELEPHONE: (212) 869-864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.3%; Score 42.8; DB 2;
87.0%; Pred. No. 1.7e-05;
tive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTT
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TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.03
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-647-655-2
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc Pattent No. 6503129
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
                                                                                                                                                                                  448269 ATCTAATCTTTTTGAAACTGAAAAGAAAACAAAAAGGATATTTTTTCA 448321
                                                                                                                  0; Gaps
                                                                      DB 4; Length 580073;
                                                                                                                                                             1 ATTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCA
                                                                 Score 25:8; DB 4; Length 5
Pred. No. 27;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
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OTHER INFORMATION: n equals a, t, c, or g
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PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08916421B Patent No. 6503729 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Methanococcus jannaschii
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCATION: (28222)
COTHER INFORMATION: n equals a, NAME/KEY: misc feature a MAME/KEY: misc (18257). (28258)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (84808) .. (84808)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
                                                                    Query Match
Best Local Similarity 67.9%;
Matches 36; Conservative
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (84808)..(848
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LENGTH: 1664976
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TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment Patent No. 6537773

TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: P8193P1

CURRENT APPLICATION WUMBER: US/08/545,528D

CURRENT FILING DATE: 1995-10-19

PRIOR PILING DATE: 1995-06-07

PRIOR PILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4824, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
                                                                                                                                                                                                                                                                                                                                                                         1422 TGTGTTTTAAATAGACAGGGGGTAAAAGAAATACAGTTCTTTTTCATGGACCA 1475
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                                                                                                                                                                                                                                                                                                                                             7 TGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGACCA
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                                                                                                                                                                                                                                                   Length 5049;
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Pred. No. 2.3;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700349086H1
US-09-313-294A-4824
                                                                                                                                                                                                                                                 Score 42.8; DB 2;
Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-545-528D-1
Sequence 1, Application US/08545528D
Patent No. 6537773
GENERAL INFORMATION:
                                                     IOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-CHITICAL: NO
                                                                                                                                                                                                                                               71.3%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.5%;
Matches 37; Conservative
5049 base pairs
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.0
Matches 47; Conservative
                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Parvovirus
                       TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .09-313-294A-4824
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LENGTH: 580073
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LENGTH: 277
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LOCATION: (319226). (319226)
COTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misor feature
LOCATION: (559167). (559167)
COTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misor feature
LOCATION: (559241). (559241)
COTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misor feature
LOCATION: (600992). (600992)
COTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misor feature
LOCATION: (622708). (622708)
COTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misor feature
LOCATION: (6227081). (6227081)
COTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misor feature
LOCATION: (657081). (657081) ö or ů UNIME/KEY: INFOGRATION: In equatis a, c, c, NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature
LOCATION: (674735)..(674435)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature
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LOCATION: (741684)..(741684)
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LOCATION: (741684)..(741684)
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature
LOCATION: (779455)..(779455) NAME/KEY: misc feature
LOCATION: (234814). (234814)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (309398). (309398)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (309418)
OTHER INFORMATION: n equals a, t, c,
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (779676)..(779676) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (312837)..(312837) OTHER INFORMATION: n equals a, t, LOCATION: (191989) ..(191989) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (234187)..(234187) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (312993)..(312993) OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, COCATION: (191955)...(191995)
OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
COCATION: (231980)...(231980)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (234220)..(234220) DTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (855539)..(855539) NAME/KEY: misc feature LOCATION: (871619)..(871619)

0; Gaps GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATANORE, HIDEMI
APPLICANT: HATANORE, HIDEMI
TILE OF INVENTION: GENOME DIA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 08135(0159)
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE PACENTIN VEY: 2.1
SEQ ID NO 1
LENGTH: 640681 Query Match 42.3%; Score 25.4; DB 4; Length 1664976; Best Local Similarity 74.4%; Pred. No. 43; Matches 32; Conservative 0; Mismatches 11; Indels 0; 0 315581 AATCAGAAAAGGCAATAAAAATATGCTGTTTTATTTAAAGAA 315623 15 AAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGA 57 NAME/KEY: misc feature
LOCATION: (1664854)..(1664855)
COTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1 σ р ö ö ö or 20 or ö ö ö c, or υÌ Sequence 1, Application US/09790988 Patent No. 6632935 NAME/KEY: misc_feature
LCCATION: (1084830). (1084830)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (105646). (1096846)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (113681). (1119881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (130881). (1310981)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (1310988). (1310988)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (1313224). (13149473)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (1343491). (1349473)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (1343491). (1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (1349491). (1470991)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LCCATION: (1349491). (1470091)
OTHER INFORMATION: n equals a, t,
CTHER INFORMATION: n equals a, t,
CTHER INFORMATION: n equals a, t,
CTHER INFORMATION: n equals a, t,
CTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (1569020). (1569020) OTHER INPORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (1602912)..(1602912) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (1603734)..(1603734) OTHER INFORMATION: n equals a, t NAME/KEY: misc feature LOCATION: (1637998)..(1637998) OTHER INFORMATION: n equals a, INFORMATION: n equals a, RESULT 8 US-09-790-988-1 a ð

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APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENCTH: 46899 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION: G
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                           GENERAL INFORMATION:
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HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-998-416-54/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
US-08-471-119A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Chumakov, Llya

APPLICANT: Chumakov, Llya

APPLICANT: Chohen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENSEI JOSOP/641,638

TITLE OF INVENTION: GENSEI JOSOP/641,638

CURRENT APPLICATION NUMBER: US/09/641,638

CURRENT FILING DATE: 2000-08-16

PRIOR FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR APPLICATION NUMBER: US 60/133,207

PRIOR PILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATTIGCTGTGTTTTAAACAGACAGAGGAGGCAAAAGAAATGCTGTTTTATTTCATGGAC 58
                                                                                                                                                                                                                                292498 TGTTTATTACGTATAAAATGGCGCAAAAAAAAGGTGTTATTTAAGG 292546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc binding
LOCATION: 482.500
OTHER INFORMATION: 12-113-276.mis2
LOCATION: 482.500
OTHER INFORMATION: 12-113-276.mis2
NAME/KEY: primer bind
LOCATION: 756.775
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 288.307
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc_binding
LOCATION: 489.513
OTHER INFORMATION: 12-113-276 potential probe
                                                                                                                                                     ö
                                                                                            Score 25; DB 4; Length 640681;
Pred. No. 50;
0; Mismatches 15; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.7%; Score 24.4; DB 4; Length 1001; Best Local Similarity 63.8%; Pred. No. 20; Matches 37; Conservative 0; Mismatches 21; Indels 0
                                                                                                                                                                                                   7 TGTGTTTTAAACAGACGAGGCAAAAGAAATGCTGTTTTATTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc binding
LOCATION: 502. 521
OTHER INFORMATION: 12-113-276.misl, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 501
OTHER INFORMATION: 12-113-276 : polymorphic base T or C
                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-641-638-310
; Sequence 310, Application US/09641638
; Patent No. 6432648
; Patent No. 6432648
; RENERAL INPORMATION:
; APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 994 TOTHER INFORMATION: n=a, g, c or t US-09-641-638-310
                                                                                            41.7%;
                                                                                            Query Match
Best Local Similarity 69.49
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
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NVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NVENTION: AND USES THEREOF
SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                           GENERAL A.C. Leitner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoergendorfer, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEB: No. 5827706artis Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100-8029/CONT/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Match
Local Similarity 63.8%; Pred. No. 46;
les 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
Sequence 1, Application US/08471119A
Patent No. 5827706
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ATCC 34921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT FILING DATE: 2003-05-06
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%; Score 23.8; DB 4; Length 8537; 66.7%; Pred. No. 51; tive 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 3; Length 716;
Pred. No. 25;
0; Mismatches 20; Indels
                                         FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/ARENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-8689
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TTTGCTGTGTTTTAAACAGACAAGGAGGCAAAAGAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
LENGTH: 8537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/10204708
Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.3%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR ESQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                      24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 34; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: PAG1015UP
US-08-998-416-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 iciacigigarigalagagargagartagaartarakarigcacititicitigarga 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%; Score 24; DB 3; Length 698; 64.3%; Pred. No. 25; clive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION TABER: US/08/997
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTONENY/AGENT INPORMATION:
NAME: Med:98, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8887
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
          ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6239264artis Corporation
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis CorSTREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-998-416-55
; Sequence 55, Application US/08998416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.0
Best Local Similarity 64.3
Matches 36; Conservative
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: PAG1015RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                  27709
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                  Sequence 3955, Application US/09328352

Releant No. 6562958

GRNERAL INFORMATION:
APPLICAMT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREBACE: Gr99-0328
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3956
LENGTH: 1335
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                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        834 TGTTAAAAACAAAGATGAAACCAAAAAACTTGCTGAATTATTTCGT 879
                                                                                                                                                                                                                                                                                                                                                   Score 23.6; DB 4; Length 1
Pred. No. 39;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TGTTTTAAACAGACAAGGAGGCAAAAGAAATGCTGTTTTATTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: Drmanac, Radoje T.
ITLE OF INVENTION: No. 6569662el Nucleic Acids and
ITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT PEPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL.FL.genes Version 1.0
LENGTH: 2549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.3%; Score 23.6; 176.3%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 567, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3956
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 69.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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Wang, Dunrui
Wang, Zhiwei
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Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps Qy 11 TTTTAAACAACAAGGGCAAAAGAAATGCTGTTTTA 48

Db 2501 TTTTAAACCAACGAGGAATAAAAAGAAATCCTGATCTA 2538
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The present sequence is a peptide fragment of parvovirus non-structure protein 1 (NS1) variant (T394A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene
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Abr43403 (Aar85384 | Aae25391 | Aae22691 | Aae2664 | Abu64764 | Abu64762 | Aae22890 | Aae22890 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aae26942 | Aa
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ADE58145
AAO11564
ADC26295
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seq length: 200000000
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Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                       463
/note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                 Parvovirus non-structure protein 1 (NS1) variant (T463A)
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                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                       AAY72710 standard; protein; 672 AA
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                                                                                                                                         (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1999;
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                                                                                                                                         06-AUG-2003
31-MAY-2001
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                                                                                                                                                                                                                                                                                                                     Parvovirus.
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                                                                                                    AAY72710;
               RESULT 3
AAY72710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                  Length 20;
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on 06-AUG-2003 to correct OS field.)
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Pred. No. 1.1e-08;
; Mismatches 0;
                                                                    100.0%; Score 113; DB 4;
100.0%; Pred. No. 2.7e-10;
Micmatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           AAY72708 standard; protein; 672 AA.
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(first entry)
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                                                                                                                                   Conservative
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Best Local Similarity
Matches 20; Conserv
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                                                Sequence 20 AA;
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31-MAY-2001
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           therapy.
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                                        The present sequence is parvovirus non-structure protein I (NSI) Vari
(T463A). The invention relates to the variants of the parvovirus non-
structure protein (NSI) having a shifted equilibrium between the DNA
                                                                                                                                                                                                                                                                                 Gaps
                              sequence is parvovirus non-structure protein 1 (NS1)
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                                                                                                                                 DNAs are useful as vectors for gene therapy.
                                                                                                                                                                                                                                          96.5%; Score 109; DB 4;
95.0%; Pred. No. 4.4e-08;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY72706 standard; protein; 672 AA.
Claim 6; Page 30-32; 41pp; English
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(first entry)
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Best Local Similarity
Matches 19; Conserv
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31-MAY-2001
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WPI; 2001-212717/22.
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                                                      N-PSDB; AAD02797
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31-MAY-2001
                             Nueesch J,
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                                                                                                                                                                                                                                                                                         The present sequence is parvovirus non-structure protein 1 (NS1) variant (T363A). The invention relates to the variants of the parvovirus nonstructure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                   Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy.
NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                        /note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                        96.5%; Score 109; DB 4; Length 672; 95.0%; Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parvovirus wild-type non-structure protein 1 (NS1).
                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                        Location/Qualifiers
                                                                                                                                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                          Claim 6; Page 19-21; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY72702 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         ICCVLNRQGGKRNTVLFHGP 400
                                                                                                                                                                                                                                                                                                                                                                                                                              1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                99EP-00115161.
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                                                                                                                                                   99EP-00115161
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                                                                                                                                                                                        Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 95.0
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                          WPI; 2001-212717/22.
                                                                Misc-difference 363
                                                                                                                                                                                                                   N-PSDB; AAD02801
                                                                                                                                                                                                                                                                                                                                                                       Sequence 672 AA;
                                                                                                                                                   13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1077260-A1
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                                                                                           EP1077260-A1
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                                                                                                              21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parvovirus.
                            Parvovirus
                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                               381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY72702;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
셤
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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                      Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 109; DB 4; Length 672;
Pred. No. 4.4e-08;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Ser substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parvovirus non-structure protein 1 (NS1) variant (S283A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72704 standard; protein; 672 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 ICCVLNROGGKRNTVLFHGP 400
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 96.5%;
Best Local Similarity 95.0%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-00115161
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(first entry)
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                                                                         Rommelaere
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7

Gaps

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Indels

4;

Score 49.5; DB 7; Pred. No. 7.4; 2; Mismatches 4;

43.8%;

Conservative

1 ICCVL----NRQG-GKRNAVLFH 18

25

Length 90;

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This invention relates to a method of identifying a compound which modulates THAP (THANCOS (death) Associated Protein)-mediated activities. The invention also relates to genes and proteins of the THAP family and uses thereof. Coordination of cell proliferation and cell death is required for normal development and tissue homeostasis in multicellular organisms. A defect in these two processes is a fundamental requirement or tunning modulate THAP1 is a pro-apoptotic protein and therapeutics which modulate THAP1 activity may be cytostatic. The sequences of the invention may prove useful for gene therapy. The method is useful for preparing a composition for treating cancer. The present sequence is the partial amino acid sequence of the human THAP4 protein which was used for homology purposes in the exemplification of the invention.
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                                                                                                                                              Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003051917-A2.
                                                                                                               Sequence 672 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens,
                                                                                                                                                                                                                                                                                                               15-JAN-2004
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                                                                                                                                                                                                                                                                                         ADD36322;
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                             THAP4
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Matches
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8X2222222288
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Query Match
Best Local Similarity
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                                                         The present sequence is parvovirus non-structure protein 1 (NSI) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as toxins for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a test compound that modulates THAP-mediated activities for treating cancer by determining whether the test compound selectively modulates the activity of the THAP-family polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAPI; human; pro-apoptotic protein; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human THAP (Thantos (death) Associated Protein) 4 partial sequence
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                                                                                                                                                                                                                                                                                                                                       Score 109; DB 4; Length 672;
Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                 Claim 6; Page 14-16; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD36322 standard; protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 ICCVLNRQGGRRNTVLFHGP 400
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                96.5%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                     THAP; THantos (death) Associated Protein; THAP family;
cell proliferation; cell death; tissue homeostasis; tumourigenesis;
THAP1; pro-apoptotic protein; cytostatic; gene therapy; cancer; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a test compound that modulates THAP-mediated activities f
treating cancer by determining whether the test compound selectively
modulates the activity of the THAP-family polypeptide.
                                                                                        Mouse orthologue to human THAP (THantos Associated Protein) Seq ID25.
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52.2%; Pred. No. 7.8;
:ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; SEQ ID NO 25; 303pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ICCAAVNCSNRQGKGEKRAVSFH 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ICCVL----NRQG-GKRNAVLFH 18
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ADD36217 standard; protein; 95
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                                                                 (first entry)
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                              (ENDO-) ENDOCUBE
                                                                                                                                                                                                                                                  WO2003051917-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 95 AA;
                                                                                                                                                                                                                   Mus musculus.
                                                                15-JAN-2004
                                                                                                                                                                                                                                                                               26-JUN-2003
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                                  ADD36217;
                                                                                                                                                                                   murine.
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RESULT 9

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antiinflammatory; thyromimetic; antiallergic; cerebroprotective;
                                                                                        Homo sapiens.
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ABR58511
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                                                                                                                                                                                                                                                                                                                                                                                                                            modulates THAP (Trancos (dearh) Associated Protein)—mediated activities. The invention also relates to genes and proteins of the THAP family and uses thereof. Coordination of cell proliferation and cell death is required for normal development and tissue homeostasis in multicallular organisms. A defect in these two processes is a fundamental requirement for tumourigenesis. THAP1 is a pro-apoptotic protein and therapeutics which modulate THAP1 activity may be cytostatic. The sequences of the invention may prove useful for gene therapy. The method is useful for amino acid sequence of a mouse orthologue of the human THAP proteins which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                   Identifying a test compound that modulates THAP-mediated activities for treating cancer by determining whether the test compound selectively modulates the activity of the THAP-family polypeptide.
                                                                                                THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAP1; pro-apoptotic protein; cytostatic; gene therapy; cancer; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; SECP; neuroprotective; relaxant; antithyroid;
antidiabetic; cytostatic; dermatological; immunosuppressive;
                                                                           Mouse orthologue to human THAP (THantos Associated Protein) Seg ID102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a method of identifying a compound which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein Incyte ID No: 7504539CD1 SEQ ID NO: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.8%; Score 49.5; DB 7; Length 205; 52.2%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                        Amalric F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; SEQ ID NO 102; 303pp; English
                                                                                                                                                                                                                                                                                                        Girard J, Roussigne M, Kossida S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ICCVL----NRQG-GKRNAVLFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD36294 standard; protein; 205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR58515 standard; protein; 548 AA
                                                                                                                                                                                                                                                                                 CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                 18-DEC-2001; 2001US-0341997P.
                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                       (ENDO-) ENDOCUBE SAS
                                                                                                                                                                                                                                                                                                                             WPI; 2003-532998/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 205 AA;
                                                                                                                                                                              WO2003051917-A2.
                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-2003
                                                      15-JAN-2004
                                                                                                                                                                                                    26-JUN-2003
                                 ADD36294;
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                                                                                                                                                                                                                                                                                   (CNRS )
                                                                                                                                   murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
ADD36294
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The invention relates to a novel isolated human secreted polypeptide (SECP). An SECP of the invention has neuroprotective, relaxant, antitipated, articipated, cytostatic, dermatological, immunosuppressive, antitihlammatory, thyromimetic, antiallergic, cerebroprotective, gastrointestinal, hepatotropic, antiallergic, cerebroprotective, gastrointestinal, hepatotropic, antiparasitic, fungicide, protozoacide, virucide, uropathic, antiparensitic, fungicide, protozoacide, virucide, uropathic, antiparensitic, fungicide, protozoacide, oricide, uropathic, antiparensitic, fungicide, protozoacide, oricide, antiparensitic, antiparensitic, fungicide, protozoacide, oricide, antiparensitic, antiparensition may have a use in gene therapy, and a polypeptide may act as either a SECP agonist or antagonist. The polypeptide are useful in diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, such as neurodegenerative disorders, muscular disorders, endocrine disorders, infections, cardiovascular disorders, or hepatic, candiovascular disorders, and disorders, and modulate the activity of SECP, and modulate the activity of SECP, and modulate the activity of SECP.
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gastrointestinal, hepatotropic, nephrotropic, anticonvulsant, fungicide, antiparkinsonian, antibacterial, antiparasitic, protozoacide, virucide, uropathic, antirheumatic, cardiant, cardiovascular, anti-HIV, nootropic, gene therapy, neurodegenerative disorder, muscular disorder, cancer, endocrine disorder, immunological disorder; gastrointestinal disorder, renal disorder, infection, cardiovascular disorder; hepatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lehr-Mason PM, Tran UK, Duggan BM;
J, Xu Y, Tang TY, Chawla NK, Elliott VS;
SD, Yao MG, Emerlian Griffin JA, Lal PG;
ghn MR, Lee GY, Ramkumar J, Gorvad AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent the human SECP's of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 166-168; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SD, Yao MG, Eme
ghn MR, Lee EA,
Borowsky ML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ICCVL----NRQG-GKRNAVLFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2001; 2001US-0326945P.
19-OCT-2001; 2001US-034371BP.
02-NOV-2001; 2001US-0343980P.
16-NOV-2001; 2001US-0332426P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002; 2002WO-US032032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thangavelu K, Yang J, Xu
Forsythe IJ, Becha SD, Y
Zebarjadian Y, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thangaver.
Forsythe IJ, Becna
Zebarjadian Y, Baughr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-371995/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Warren BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACC72453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                      WO2003029437-A2
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2

Gaps

5

08-JUL-2003

ABR58511;

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Forsythe IJ, Becha
Zebarjadian Y, Baug
Kable AE, Lu DAM,
                                                                                    WPI; 2003-371995/35.
                                                                                      N-PSDB; ACC72449
                                                                                                                                                       Sequence 577 AA;
                                           WO2003029437-A2.
                                               10-APR-2003
                                                                                               e.g. neurc
infection.
                                                                                                                                                            Query Match
                                       Ношо
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This invention relates to a method of identifying a compound which modulates THAP (THANCOS (death) Associated Protein)-mediated activities. The invention also relates to genes and proteins of the THAP family and uses thereof. Coordination of cell proliferation and cell death is required for normal development and tissue homeostasis in multicellular organisms. A defect in these two processes is a fundamental requirement for tumourigenesis. THAP1 is a pro-apoptotic protein and therapeutics which modulate THAP1 activity may be cytostatic. The sequences of the invention may prove useful for gene therapy. The method is useful for preparing a composition for treating cancer. The present sequence is the amino acid sequence of the human THAP4 protein which is related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THAP; THantos (death) Associated Protein; THAP family; cell proliferation; cell death; tissue homeostasis; tumourigenesis; THAP1; human; pro-apoptotic protein; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.5; DB 7; Length 577;
Pred. No. 52;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a test compound that modulates THAP-mediated treating cancer by determining whether the test compound modulates the activity of the THAP-family polypeptide.
                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Human THAP (THantos (death) Associated Protein) 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Girard J, Roussigne M, Kossida S, Amalric F;
     d. No. 52;
Mismatches
     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; SEQ ID NO 6; 303pp; English
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                                                                                  18
                                                                                                                                                                                                                                                                       ADD36198 standard; protein; 577 AA
                                                                                  1 ICCVL----NRQG-GKRNAVLFH
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|CCAAVNCSNRQGKGEKRAVSFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001; 2001US-0341997P.
  ilarity 52.2%;
Conservative
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N-PSDB; ADD36355, ADD36442.
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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tes 12; Conserv
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003051917-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                12;
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                                                                                                                                                                                                                                                                                                                           ADD36198;
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ADD36198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated human secreted polypeptide (SECP). An SECP of the invention has neuroprotective, relaxant, antithyroid, antidiabetic, cytostatic, dermatological, immunosupressive, antinilammatory, thyromimetic, antiallergic, cerebroprotective, gastrointestinal, hepatotropic, nephrotropic, anticonvulsant, antiparterial, antiparasitic, fungicide, procacide, vircide, uropathic, antirheumatic, cardiant, cardiovascular, anti-HHV, and nootropic activity. A polymotleotide of the invention may have a use in gene therapy, and a polymeptide may act as either a SECP agonist or antagonist. The polypeptide or its fragments, and the polymeticelectide encoding the polypeptide are useful in diagnosing, preventing, and treating disorders associated with an abnormal expression.
                                                                                                                                                                                                                                                 antidiabetic; cyfostatic; dermatological; immunosuppressive; antinflammatory; thyromimetic; antiallergic; cerebroprotective; asstrontestinal; hepatotropic; nephrotropic; anticonvulsant; fungicide; antipartkinsonian; antibacterial; antiparasitic; protozoacide; virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV; nootropic; gene therapy; neurodegenerative disorder; muscular disorder; cancer; endocrine disorder; immunological disorder; gastrointestinal disorder; renal disorder; hepatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and
                                                                                                                                                                                                                        secreted protein; SECP; neuroprotective; relaxant; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yue H, Warren BA, Lehr-Mason PM, Tran UK, Duggan BM;
Thangavelu K, Yang J, Xu Y, Tang TY, Chawla NK, Elliott VS;
Forsythe IJ, Becha SD, Yao MG, Emerling BM, Griffin JA, Lal PG;
Zebarjadian Y, Baughn MR, Lee EA, Lee SY, Ramkumar J, Gorvad AE;
                                                                                                                                                                 Human secreted protein Incyte ID No: 7503072CD1 SEQ ID NO: 23.
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                   577
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19-OCT-2001; 2001US-0343718P.
02-NOV-2001; 2001US-0343980P.
16-NOV-2001; 2001US-0332426P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002; 2002WO-US032032
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                   ABR58511 standard; protein;
                                                                                                                        (first entry)
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activities for selectively

5

Gaps

5,

RESULT 13

AAW13494

DB 6; Length 577;

43.8%; Score 49.5;

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chronic constriction injury; CCI; spared nerve injury; SNI; Chung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 298 AA;
                                                                                                                                                                                                                                              GENBANK; S32426.
                                                WO2003016475-A2
                                                                       27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA011564;
                                                                                                                                                                                                        Woolf C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The herpes helper virus (HHV-6) transcription suppressor (ts) gene shuts off transcription of the HIV long terminal repeat promoter and of the H-ras gene. A new gene therapy method for treating a subject at risk of or sulfering from a disease state associated with oncogenic transformation or lentivirus infection comprises delivering a vector comprising a polymucleotide sequence encoding a transcription suppressor (especially the HHV-6 ts gene) to the patient's cells. The method is used for the prevention and treatment of viral cancers and lentivirus (especially infection. Cancers which may be treated include those caused by members of the ras oncogene family and cancers associated with human papilloma virus (HPV), bovine papilloma virus (BPV) and HTLV-1 (human papilloma virus (HPV) to some papilloma virus (BPV) and HTLV-1 (human for cell lymphotropic virus-1). The present sequence is the protein encoded by the HHV-6 ts gene; it can be used directly to treat the same diseases.
                                                                                                                                                                                                                                                                                                                                                                                 Gene therapy for treatment of viral cancers or lentivirus infection - by transfection of cells with transcription suppressor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
                                                                                                         Transcription suppression; human cancer; ts gene; transformation; herpes helper virus; HHV-6; ras oncogene family; lentivirus; human appilloma virus; HPV; bovine papilloma virus; BPV; human T cell lymphotropic virus-1; HTLV-1; HTV LTR promoter; infection; human immunodeficiency virus; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.4%; Score 49; DB 2; Length 490; 56.2%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                    HHV-6 transcription suppressor protein.
                                                                                                                                                                                                                                                                                                                                   Rosenthal LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Protein S32426, SEQ ID NO 4016.
 AAW13494 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE58145 standard; protein; 298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2A; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 LSHRGGKKNTVSFIGP 339
                                                                                                                                                                                                                                                                                   95US-0001010P.
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                                                            (first entry)
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                                                                                                                                                                                                                                                                                                          (GEOU ) UNIV GEORGETOWN
                                                                                                                                                                                                                                                                                                                                   Araujo JC, Doniger J,
                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-118825/11.
                                                                                                                                                                                    Human herpesvirus 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 490 AA;
                                                                                                                                                                                                         409702841-A1
                                                                                                                                                                                                                                                           09-JUL-1996;
                                                                                                                                                                                                                                                                                   10-JUL-1995;
                                                27-AUG-2003
21-OCT-1997
                                                                                                                                                                                                                                   30-JAN-1997
                         AAW13494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE58145;
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ADE58145
 5×5×5×8×8
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polymeptides or their antibodies. The polynucleotide or the compound to injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English
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                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                              14-AUG-2002; 2002WO-US025765
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Rattus norvegicus
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to pyrokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammanomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or readment of canner, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                         Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 25456; 1399pp + Sequence Listing; English.
                   Human polypeptide SEQ ID NO 25456.
                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI91495.
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                                                                                                                                                                                                     WO200164835-A2.
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                              07-SEP-2001.
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Query Match 41.6%; Score 47; DB 4; Length 99; Best Local Similarity 46.7%; Pred. No. 20; Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps

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2 CCVLNRQGGKRNAVL 16 ||::| | | | 43 CCIINNSNGNRTIVL 57

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Search completed: May 28, 2004, 12:57:04 Job time: 48.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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1: pir1:*
2: pir2:*
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No.
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Query Match 96.5%; Score 109; DB 1; Length 672; Best Local Similarity 95.0%; Pred. No. 8.8e-10; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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1 ICCVLNRQGGKRNAVLFHGP
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Local Similarity 90.0%;
les 18; Conservative 0
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90.0%;
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UYPVIM

noncapta disperies minute virus of mice (strain MVMi)

C;Species: minute virus of mice, murine parvovirus

C;Species: minute virus of mice, murine parvovirus

C;Species: minute virus of mice, murine parvovirus

C;Species: minute virus of mice, murine parvovirus

C;Species: minute virus of mice, murine parvovirus

C;Species: minute virus of mice, murine parvovirus

C;Species: minute virus of mice, murine parvovirus

R;Sahli, R.; McMaster, G.K.; Hirt, B.

R;Sahli, R.; McMaster, G.K.; Hirt, B.

Nucleic Acids Res. 13, 3617-3633, 1985

A;Title: DNA sequence comparison between two tissue-specific variants of the autonomous A;Residues: 1-721 < SAH>

A;Residues: 1-721 < SAH>

A;Residues: 1-721 < SAH>

A;Residues: 1-721 < SAH>

A;Residues: 1-721 < SAH>

A;Title: DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and G;A;Residues: A29510; MUD:86115415; PMID:3352703

A;Accession: A29510; MUD:86115415; PMID:335289; PIDN:AA69566.1; PID:9825477

C;Superfamily: parvovirus noncapsid protein

C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Concapsid protein NSI - feline panleukopenia virus (fragment)
C;Species: feline panleukopenia virus, FPLV
C;Species: feline panleukopenia virus, FPLV
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
R;Carlson, J; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J, Virol. 55, 574-587, 1985
Jyitle: Cloning and sequence of DNA encoding structural proteins of the autonomous parv A;Reference number: A03697; MuID:85265017; PMID:2991581
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Pred. No. 8.8e-10;
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95.0%; Pred. No. 9.4e-10;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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A,Cross-references: EMBL.V01115
C,Superfamily: parvovirus noncapsid protein
C,Keywords: noncapsid protein
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noncapaid protein NS1 - mink enteritis virus (strain Abashiri)

C)Species: mink enteritis virus, MEV
C)Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C)Accession: A38350
R;Kariatsumari, T. Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinage J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the A;Reference number: A38350; MUID:91202123; PMID:2016597
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-bec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A36608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: canine parvovirus (strain N)
C;Species: canine parvovirus, CPV
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A2962
R;Reed, A.P.; Jones, E.V.; Miller, T.J.
J. Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine parvovirus.
A;Reference number: A29962; MUID:88062992; PMID:2824850
A;Molecule type: DNA
A;Residues: 1-392 <CAR>
A;Residues: 1-392 <CAR>
A;Cross-references: EMBL:M10824; NID:g333474; PIDN:AAA47160.1; PID:g333475
C;Superfamily: parvovius noncapsid protein
C;Keywords: noncapsid protein
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A,Molecule type: DNA
A,Residues: 1-668 <REE>
A,Cross-references: EMBL:M19296; NID:g333438; PIDN:AAA67459.1; PID:g333439
C,Superfamily: parvovirus noncapsid protein
C,Keywords: noncapsid protein
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C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Pred. No. 2.6e-08;
0; Mismatches 2; Indels
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tive 0; Mismatches 2.
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Pred. No. 1.6e-08;
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0; Mismatches

88.5%; 90.0%;

Best Local Similarity 90.0 Matches 18; Conservative

Query Match

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NAIternate names: left-ORF protein
C;Species: Aleutian mink disease virus
C;Accession: A36760; A35529
R;Bloom, M.E.; Alexandersen, S.; Perryman, S.; Lechner, D.; Wolfinbarger, J.B.
J. Virol. 62, 2903-2915, 1988
A;Fitle: Nucleotide sequence and genomic organization of Aleutian mink disease parvovirus
A;Reference number: A36760; MUID:88275062; PMID:2839709
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A;Description: Sequence comparison of the non-structural genes of four different types of A;Reference number: S41434
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C;Date: 15-Sep-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C;Accession: S41861; S41436
                                                                                A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-62 <BER>
A;Residues: 1-62 <BER>
A;Experimental source: strain NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138790)
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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    A; Reference number: A48472; MUID: 94025614; PMID: 8212598
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444 LCTILTKQGGKRGCIWFYGP 463
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A; Residues: 1-620 <BL2>
A; Cross-references: EMBL:M20036
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Matches 10; Conservative
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Matches 10; Conserv
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A Molecule type: DNA
A; Residues: 1-641 <GOT>
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                                                     A;Accession: A48472
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R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Virol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvo
A;Reference number: A36608; MUID:91073139; PMID:2174965
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A Mesidues: 1-660 cRAN-
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C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Accession: A36217; A48472; A33743
R;Vasudevacharya, J; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Accession: A36217; MUID:91021005; PMID:2219713
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A;Residues: 1-85,'R',87-273,'R',275-375,'V',377-620,'NLH',623-624,'PTPPD',630,'AIR',634,
A;Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and translation products of
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C;Daces 30-26p-1991 #sequence revision 30-Sep-1991 #text_change 16-Jun-2000
C;Accession: A33302; A33743; A36217
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol, 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
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A;Experimental source: strain NADL-2
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                                                                                                                                                                      A,Accession: A36608
A;Molecule type: DNA
A;Residues: 1-668 <MAR>
A;Cross-terences: GB:X55115; NID:g60863; PIDN:CAA38910.1; PID:g60864
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Pred. No. 2.6e-08;
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Best Local Similarity 85.0%; Pred. No. 5.5e-08;
Matches 17; Conservative 1; Mismatches 2; Indels
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380 ITCVLNRQGGKRNTILFHGP 399

A; Residues: 1-662 <VAS> A; Molecule type: DNA

1 ICCVLNRQGGKRNAVLFHGP 20

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Gaps

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Length 726; 2; Indels

Score 55; DB 1; Pred. No. 0.69; 6; Mismatches

20

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Search completed: May 28, 2004, 13:00:58 Job time : 10.5 secs
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295 MLSKKTGKRNSTLFYGP 311
Query Match
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Matches 9; Conservative
                                                                                                                        4 VLNRQGGKRNAVLFHGP
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A,Cross-references: EMBL.M14363; NID:g333454; PIDN:AAB59845.1; PID:g808803; EMBL:M21972;
C,Superfamily: parvovirus noncapsid protein
C,Keywords: noncapsid protein
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A. Description: Sequence comparison of the non-structural genes of four different types of A. Reference number: S41434
A. A. Status: preliminary
A. Solutus: preliminary
A. Molecule type: DNA
A. Residues: 1-641 < GOT>
                                                                                                                                                                          Nicottechald, E.; Alexandersen, S.; Storgaard, T.; Bloom, M.E.; Aasted, B. submitted to the EMBL Data Library, January 1994
A. Description: Sequence comparison of the non-structural genes of four different types A; Reference number: S41434
A; Reference number: S41434
A; Reference prealinary
A; Accession: S41439
A; Residues: prealinary
A; Residues: 1.641 < COT>
A; Residues: 1.641 < COT>
A; Conserreferences: EMBL: Z29576
C; Genetics: S86/1
C; Superfamily: parvovirus noncapsid protein
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OUTPVS1

CONCAPAST 15

OUTPVS1

CONCAPAST 1- bovine parvovirus

C.Species: bovine parvovirus

C.Species: bovine parvovirus

C.Species: bovine parvovirus

C.Species: bovine parvovirus

C.Species: bovine parvovirus

C.Species: bovine parvovirus

C.Species: bovine parvovirus

C.Species: Bovine parvovirus

C.Species: Bovine 1999

C.Species: Bovine 1999

C.Species: Bovine parvovirus

A.Title: Complete nucleotide sequence and genome organization of bovine parvovirus.

A.Reference number: A26104; MUID:87061184; PMID:3783814
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;Species: Aleutian mink disease virus
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Feb-1997
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C;Species: Aleutian mink disease virus
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Pred. No. 0.03;
4; Mismatches 6; Indels
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P03133 hamster par
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P12929 canine parv
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P24030 aleutian mi
P07296 bovine parv
P2419 human papil
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Q02973 mas musculu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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VEI HPV36 VEI HPV17 HS70 ACHKL HS70 BRELC YDBH ECOLI EB30 CAREL MYH7 PIG MYH7 PIG MYH7 PIG RY	ALIGN	RD; PRT; 66 Created) Last sequence upc Last sequence upc 1 (Nonstructural n	roviridae	[1] SEQUENCE FROM N.A. MEDLINE=93297126; PubMed=8517025; Diffoot N., Chen K.C., Bates R.C., Lederma M. "The complete nucleotide sequence of parvovi localization of a unique sequence possibly rencapsidation pattern."; Virology 192:339-345(1993)!- FUNCTION: Seems necessary for viral DNA -!- STUNCTION: Seems necessary for viral DNA -!- SIMILARITY: Belongs to the parvoviruses	This SWISS-PROT entry is copyright. It is phetween the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. Entities requires a license agreement (See or send an email to license@isb-sib.ch).	ED_CDS. IS1. ATP (PO' 7; CAE69	Score 109; Pred. No. 5 0; Mismatch	3P 20 1P 400	PRT; 672 AAed) ed) sequence update) annotation update
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. 444444444444444444444444444444444444	•	PAVL 1; N-19 N-19 C-19	NS1. Parvovirus LuIII. Viruses; 88DNA viruses	SEQUENCE FROM N.A. MEDLINE=93297126; PubMed. Diffoot N., Chen K.C., B. "The complete nucleotide localization of a unique encapsidation pattern."; Virology 192:339-345(199; -i - FUNCTION: Seems nece: -i - SIMILARITY: Belongs in	This SWISS-PROT entry is copbetween the Swiss Institute the European Bioinformatics use by non-profit institute modified and this statement entities requires a license or send an email to licensed	P-P-	atch Sal	381 10	0.1 C-1-1
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"DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:3617-333(1985).
-: FUNCTION: Seems necessary for viral DNA replication.
-: SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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MEDLINE=86115415; PubMed=3502703;
MEDLINE=86115415; PubMed=3502703;
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MEDLINE=86115415; PubMed=3502703;
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Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
                                                                                         Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Pred. No. 5.5e-10;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
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Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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25F025FE328B4DF0 CRC64;
                                                              Murine minute virus (strain MVMi) (Murine parvovirus)
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EMBL; M12032; AAA69567.1; -.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
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MEDLINE=85242059; PubMed=3855242;
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76140 MW;
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J. Virol. 57:656-669(1986)
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Best Local Similarity 95.0
Matches 19; Conservative
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672 AA;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
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use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10799;
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1-JUL-19966 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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PIR, A03696; UYPV1M.
TRANSPAC; T02375; -.
Interpro; PRR01057; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; T.
Nonstructural protein; Noncapsid protein; DNA replication;
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75993 MW; 12F331142F72AA6D CRC64;
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95.0%; Pred. No. 5.5e-10;
tive 0; Mismatches 1;
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Pfam; PF01057; Parvo NS1; 1.
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76248 MW;
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                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Gen. Virol. 72:867-875(1991).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                         Virology 183:195-205(1991).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Construction and nucleotide sequence analysis of an infectious DNA
                                                                                                                             "Mapping specific functions in the capsid structure of canine
parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91202123; PubMed-2016597;
Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.
Goto H., Shinagawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses, seDNA viruses, Parvoviridae, Parvovirinae, Parvovirus
NCBI_TaxID=10793;
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1-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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23 N -> D (IN REF. 2).
21 I -> V (IN REF. 2).
275 I -> N (IN REF. 2).
76768 MW; 4F8FEA3EEG2D2AE7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Gen. Virol. 71:2747-2753(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 IACVLNROGGKRNTVLFHGP 401
                                                                                    MEDLINE=91272479; PubMed=1647068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A36608; UYPVFP.
InterPro; IRRO03593; AAA ATPase.
InterPro; IPR001257; Parvo NSI.
Pfam; PP01057; Parvo_NSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X55115; CAA38910.1; -. EMBL; M38246; AAC37927.1; -.
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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443
575
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575
668 AA;
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                                          SEQUENCE FROM N.A.
                                                                                                             Parrish C.R.;
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P27438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85265017; PubMed=2991581;
Carlson J., Rushlow K., Maxwell I., Maxwell F., Winston S., Hahn W.;
"Cloning and sequence of DNA encoding structural proteins of the
autonomous parvovirus feline panleukopenia virus.";
J. Virol. 55:574-587(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"Nucleotide sequence of feline panleukopenia virus: comparison with
canine parvovirus identifies host-specific differences.";
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                                                                                                                                                                                                                                                                       Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBL_TaxID=10786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feline panleukopenia virus (strain 193) (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.5%; Score 100; DB 1; Length 392; 90.0%; Pred. No. 9.2e-09; ive 0; Mismatches 2; Indels
                                                                                                                             Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ATP (POTENTIAL).
43971 MW; B875ADDB4977F616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         668 AA.
                                                                                       392 AA
                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=193/70;
MEDLINE=91073139; PubMed=2174965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A03697; UYPVIF.
InterPro; IPRO013593; AAA ATPase.
InterPro; IPRO01257; Parvo_NSI.
Pfam; PF01057; Parvo_NSI; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ICCVLNROGGRRNAVLFHGP 20
                                                                                                                                                                                                                                                            Feline panleukopenia virus (FPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M10824; AAA47160.1; -.
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les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 1
392 AA;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      (Fragment).
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P24842;
                                                              VNCS_FPV
ID _VNCS_FPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parrish C.R.;
Submitted (NG-1990) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Geems necessary for viral DNA replication.
-i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88062992; PubMed-2824850;
Reed A.P., Jones E.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
J. Virol. 62:266-276(1988).
                                                                                                                                                                                                                                                                                                                                                            Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
DE2CCEA69D2A63A6 CRC64;
                                                                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                      668 AA
                                      PRT;
                                                                                                                                                                                                                                                                                                                      Canine parvovirus (strain N) (CPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M19296; AAA67459.1; -.
EMBL; M38245; AAB02798.1; -.
PIR; A29662; UYEVCP.
Interpro; IPR003593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 AT
76764 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE 90085785; PubMed=2596019; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; Lerminal palindrome of porcine parvovirus, strain NADL-2."; Virology 173:368-377(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family
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G -> R (IN REF. 2).

K -> R (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNTDT -> NIHLTPTPPDSAIRTP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91021005; PubMed=2219713;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
"The complete nucleotide sequence of an infectious clone of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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MEDLINE=90010964; PubMed=2794971;
Ranz A.I., Manclus J.J., Diaz-Aroca E., Casal J.I.;
Ranz Parcovinus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 98; DB 1; Length 660;
85.0%; Pred. No. 3.4e-08;
iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001257; Parvo NS1.
Pfam, PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COB1DF2226A2EF0A CRC64;
                                                                                                                                                                                                                                P18847; P22965;
01-NOV-1990 (Rel. 16, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                     660 AA.
382 IACVLNROGGKRNTVLFHGP 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parvovirus, strain NADL-2.
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                         STANDARD;
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376
621
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                                                                                                                                                                                                            VNCS PAVPN
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RESULT 10

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Gaps

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Length 668;

88.5%; Score 100; DB 1; Length 66 90.0%; Pred. No. 1.6e-08; ive 0; Mismatches 2; Indels

Query Match
Best Local Similarity 90.0
Matches 18; Conservative

1 ICCVLNRQGGKRNAVLFHGP 20

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                                                                     is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
  the Swiss Institute of Bioinformatics and the EMBL outstation
use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine parvovirus (BPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide sequence and genome organization of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87061184; PubMed=3783814;
Chen K.C., Shull B.C., Moses E.A., Lederman M., Stout E.R.,
Bates R.C.;
                                                                                                                                                                                                                                                                                                                                                                  Length 590;
                                                                                                                                                                                                   InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.7%; Score 55; DB 1; Length 726; 52.9%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                . Match 60.2%; Score 68; DB 1; Length 590 Local Similarity 50.0%; Pred. No. 0.0023; es 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                            439 ATP (POTENTIAL).
67364 MW; 9898818AFD5343B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 317 ATP (POTENTIAL).
726 AA; 81189 MW; 42659A611A3AF038 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1988 (Rel. 07, Created)
1-APR-1988 (Rel. 07, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncappid protein NS-1 (Nonstructural protein NS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 AA
                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| :| :||||| : |:||
414 LCTILTKQGGKRGCIWFYGP 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ICCVLNRQGGKRNAVLFHGP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|:::||||:|||
295 MLSKKTGKRNSTLFYGP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                            EMBL; M20036; AAA66612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parvovirus.";
J. Virol. 60:1085-1097(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M14363; AAB59845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VLNRQGGKRNAVLFHGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                 439
                                                                                                                                                                                 PIR; A36760; UYPVAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; C26104; UYPVS1.
                                                                                                                                                                                                                                                                                                                      590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10784;
                                                                                                                                                                                                                                                                                                 432
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                                                                                                                                                                                                                                                                       ATP-binding
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                              NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P07296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
VNCS_PAVBO
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation let buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long a sits content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                            MEDLINE=96183900; PubMed=8642680;
Bergeron J., Hebert B., Tijssen P.;
Bergeron J., Hebert B., Tijssen P.;
Bergeron J., Hebert B., Tijssen P.;
Identification of the Allotropic determinant and comparison with those of NADL-2 and field isolates.";
J. Virol. 70:2508-2518(1996).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence and genomic organization of Aleutian mink disease parvovirus (ADV): sequence comparisons between a nonpathogenic and a pathogenic strain of ADV."; J. Virol. 62:2903-2915(1988): -i- FUNCTION: Seems necessary for viral DNA replication.
-i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aleutian mink disease parvovirus (strain G) (ADV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 86.7%; Score 98; DB 1; Length 662; Local Similarity 85.0%; Pred. No. 3.4e-08; les 17; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TP (POTENTIAL).
B53F76D9F9FBD613 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88275062; PubMed=2839709;
Bloom M.E., Alexandersen S., Perryman S., Lechner D.,
                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapaid protein NS-1 (Nonstructural protein NS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 AA.
                           662 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                   Porcine parvovirus (strain Kresse) (PPV)
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 ITCVLNRQGGKRNTILFHGP 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001257; Parvo NS1. Pfam; PF01057; Parvo NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U44978; AAC40229.1; -.
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                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 AA;
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=73487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10783;
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VNCS ADVG
ID VNCS ADVG
AC P24030;
                           PAVPK
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Matches
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Gaps

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                                                                            Astrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Mochan P.J., McKarnan K.J., Mallek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young M., Green E.D., Dickson M.C.,

Rhiching M., Madan A., Young W., Green E.D., Dickson M.C.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska W., Sanilus D.E.,

Menterfield Y.S.N., Krzywinski W.I., Marra M.A.,

Rochneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE OF 221-577 FROM N.A.

SEQUENCE OF 221-577 FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugino S., Shiratori A., Sudo H., Sudo H.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,

Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabo S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

Ninomiya K., Iwayanagi T.;

Submitted (FEB-2000) to the BMBL/GenBank/DDBJ databases.

-- SIMILARITY: Contains 1 THAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE OF 221-577 FROM N.A.
MEDLINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lai C.-Hication of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49.5; DB 1; Length 577;
Pred. No. 2.3;
2; Mismatches 4; Indels 5
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R -> M (IN REF. 3 AND 4).

R -> M (IN REF. 4).

40660A5ACDD0A7C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BC000247; AAH00247.1; ALT_INIT.
EMBL; BC00439, AAH09439.1; ALT_INIT.
EMBL; AX001216; BAA91560.1; ALT_INIT.
EMBL; AR32970; AAD27745.1; --
                                            TISSUE=Brain, and Eye;
MEDLINE=22388257; PubMed=12477932;
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Pfam; PF05485; THAP; 1.
SMART; SM00692; DM3; 1.
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                   58-577 FROM N.A.
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Matches 12; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                      MEDLINE=90281611; PubMed=2162112; MEDLINE=90281611; PubMed=2162112; Adachi A., Ishibashi M.; Kiyono T., Adachi A., Ishibashi M.; Kiyono T., Adachi A., Ishibashi M.; Genome organization and taxonomic position of human papillomavirus type 47 inferred from its DNA sequence."; Virolegy 177:401-405(1990).
-1. FUNCTION: ATP-DEPRMENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2 PROTEIN THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS.
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Pfam; PF00524; E1 N; 1.
Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Wan D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gu J.R.; "Novel human cDNA clones with function of inhibiting cancer cell growth."; (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage, Papillomaviridae;
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70010193AE041730 CRC64;
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                                                                                                  (Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 36, Last annotation update)
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                                                      605 AA.
                                                        PRT;
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PIR; C35324; W1WL47.
InterPro; IPR001177; Papillom_E1.
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                                                                                                                                                                                                                  Human papillomavirus type 47.
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                                                      STANDARD;
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                                                                                                                                                                             Replication protein El.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein.
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                                                                                                                                                                                                                                                                             Papillomavirus
                                                                                                          01-AUG-1991
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15-JUL-1998
                                                      VE1 HPV47
P22419;
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RESULT 13

VEL HPV47

ID P241

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RESULT 14 THA4 HUMAN

Matches

THAP4.

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Gaps

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-!- SIMILARITY: TO DNA REPLICATION PROTEIN (REP) OF ADENO-ASSOCIATED VIRUS 2 (AC P03132).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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MEDLINE=95266321; PubMed=7747482;
Gompela U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
"The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91226542; PubMed=1851252;
Thomson B.J., Efstathiou S., Honess R.W.;
"Acquisition of the human adeno-associated virus type-2 rep gene by human herpesvirus type-6.";
Nature 351:78-80(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92333248; PubMed=1321205;
Thomson B.J., Honess R.W.;
Thomson B.J., Honess R.W.;
The right end of the unique region of the genome of human herpesvirus 6 U1102 contains a candidate immediate early gene enhancer and a homologue of the human cytomegalovirus US22 gene
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Pred. No. 2.4;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              U94 OR REP OR HCLF2.
Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; deDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10370;
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InterPro; IPR01257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 490 AA; 55848 MW; 221CE58165187C1F CRC64;
                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                          490 AA.
                                       3 ICCAAVNCSNRQGKGEKRAVSFH 25
1 ICCVL----NROG-GKRNAVLFH 18
                                                                                                                                                                                                                                          PRT;
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J. Gen. Virol. 73:1649-1660(1992)
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56.2%;
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Best Local Similarity 56.2
Matches 9; Conservative
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08120 leptospira
067671 goose parvo
08128 muscovy duc
065443 barbarie du
06765 goose parvo
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Ball-Goodrich L.J., Johnson E., Jacoby R.;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
Bivergent replication kinetics of two phenotypically different parvoviruses of rate;
J. Gen. Virol. 82:537-546(2001).
EMBL; AF317513; AAK27438.1;
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
NON_TER
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=155025;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Nonstructural protein 1 (Fragment)
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Copyright (c) 1993.- 2004 Compugen Ltd.
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1 ICCVLNRQGGKRNAVLFHGP 20
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                            Kilham rat virus.
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                                                                                                                           Kilham rat virus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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NCBI_TaxID=172385;
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Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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EMBL; AF332882; AAM3275.1; -.

Interpro; IPRO01257; Parvo NSI.

Pfam; PF01057; Parvo NSI; I.

SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
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Last annotation update)
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                    Nonstructural protein (Fragment).
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InterPro; IPR001257; Parvo NSI.
Pfam; PF01057; Parvo NSI; I.
NON TER
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Twirnl 72:3289-3299(1998).
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Q8JV18;
01-OCT-2002 (TEMBLrel. 22,
01-OCT-2002 (TEMBLrel. 22,
01-MAR-2003 (TEMBLrel. 23,
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Matches 19; Conservative
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RESULT 3

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RESULT 4
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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NCBI_TaxID=35340;
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ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus,
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                                                                                                                                                                                                                                                                                                                                                            Length 672;
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                                                                                                                             Brown D.W., Like A.A.; "Sequence of a Diabetogenic Parvovirus of Rats."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ball-Goodrich L.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;
                                                                                                                                                                                                                EMBL; U79033; AAB38326.1; -.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; \(\overline{1}\).
SEQUENCE 672 AA; \(\overline{7}\)6201 MW; C2F1A71F6EF449A6 CRC64;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=172386;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172387;
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SEQUENCE FROM N.A.

MEDLINE-22120170; Pubmed=12124471;
WAN C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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MEDLINE=22120170; PubMed=12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                          parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
BMBL, AR321230, AAM93272.1;
Interpro; IRR01257; Parvo NS1.
Pfam; PP01057; Parvo NS1; I.
SEQUENCE 672 AA; 75987 MW; 2284611C20CDB6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
BMBL; AR332884; AAM93279.1; -.
Interpc; IRR001257; Parvo NS1.
Pfam; PP01057; Parvo NS1; I.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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J. Gen. Virol. 83:2075-2083 (2002).
EMBL; AF332883; AAM93277.1; -.
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Q8JV16
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MEDLINE=87061199; PubMed=3783817;
MCGAD W.R., Ward D.C.;
"Three splicing patterns are used to excise the small intron common all minute virus of mice RNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MVM(p);
MEDLINE=86115415; PubMed=3502703;
AREDLINE=86115415;
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MVM(p);
MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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96.5%; Score 109; DB 12; Length 672; 95.0%; Pred. No. 7.1e-10; ive 0; Mismatches 1; Indels (
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EMBL, J02275; AAA67108.1; -.

INCEPPO; IPRO01257; Parvo NS1.

SEQUENCE 721 AA; $1896 MW; 18391758E42FODCF CRC64;
                                                                                                                                                                                                                                                                                                                                      Q84365;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Nonstructural protein.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                               721 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 AA
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Nucleic Acids Res. 11:999-1018(1983)
                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                     381 ICCVLNRQGGRRNTVLFHGP 400
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                                                                                                               1 ICCVLNRQGGKRNAVLFHGP 20
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prototype strain.";
J. Virol. 57:656-669(1986).
                               Local Similarity 95.0 es 19; Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Gaps

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"Evolutionary pattern of feline panleukopenia virus differs from that of canine parvovirus.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

EMBL, AB000057; BAADBL:
GO, GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR00159; AAA ATPase.
InterPro; IPR001297; Parvo NS1.
InterPro; PF01057; Parvo NS1.
SWART; SM00382; AAA; 1.
SRAWRT; SM00382; AAA; 1.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Feline panleukopenia virus (FPV).
Viruses, sabNa viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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                                                                                                                                                                                                                                                                                                                                                                                      Length 668;
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
REBL; AB0000669; BAA19030.1; -.
REG) GO:0001069; BAA19024.1; -.
RGO; GO:000166; F:nucleotide binding; IEA.
RINterPro; IPR00153; AAA ATPase.
R InterPro; IPR00157; Parvo_NS1.
R Pfam; PF01057; Parvo_NS1.
R SMART; SM0382; AAA; 1.
Nonstructural protein.
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 2.4e-08;
0; Mismatches 2;
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Matches 18; Conservative
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nes 18; Conservative
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Feline panleukopenia viri
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SEQUENCE FROM N.A.
STRAIN=PLI-IV;
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                                                                             Horiuchi M.;
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"Evolutinary pattern of feline panleukopeina virus differs that of
                                                                                                                                   STRAIN=lymphotropic variant;
MEDLINE=86115415; PubMed=3502703;
MEDLINE=86115415; PubMed=3502703;
MEDLINE=86115415; PubMed=3502703;
MEDLINE-86115415; PubMed=3502703;
MUM (1), and comparison with the DNA sequence of the fibrotropic wariant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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                             Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                                                                                                                                                           prototype strain.";
J. Virol. 570:656-669(1986).
EMBL; M12032; AAA69566.1; -.
PIR; A23008; UPVIM.
InterPro; IRR01127; Parvo NS1.
Pfam; PP01057; Parvo NS1.
SEQUENCE 721 AA; 81863 MW; 9FD29C327C7F4BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76755 MW; 37ABDFD347017F52 CRC64;
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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90.0%; Pred. No. 2.4e-08;
cive 0; Mismatches 2;
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96.5%; Score 109; DB 12;
Best Local Similarity 95.0%; Pred. No. 7.6e-10;
Matches 19; Conservative 0; Mismatches 1;
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EMBL; AB000062; BAA19023.1; -
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR0013593; AAA ATPase.
InterPro; IPR001257; Parvo NSI.
Pfam; PR01057; Parvo NSI.
SMART; SM00382; AAA; I.
SEQUENCE 668 AA; 76755 MW; 37ABDFD3470
        minute virus (Murine parvovirus)
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Feline panleukopenia virus (FPV)
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Best Local Similarity
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                                                                                                             SEQUENCE FROM N.A.
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                                                     NCBI TaxID=10794;
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01-MAY-1997
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OS Felin
OC Virus
OX NCBL
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae, Parvovirus.
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88.5%; Score 100; DB 12; Length 668;
Best Local Similarity, 90.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels (
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                                                       Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

REMBL; AB000065; BAA19028.1; ---
REMBL; AB000065; BAA19028.1; ---
REGO; GO:0019012; C:virion; IEA.

RGO; GO:00166; F:nucleotide binding; IEA.

RINEEPRO; IPR001257; PAPA ATPASS.

RINEEPRO; IPR001257; PAVO NS1.

R SMART; SMOS1382; AAA, 1.

R SMART; SMOS1382; AAA, 1.

R NOMBTULUMAL PROCESH.

SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, #AB000015;
EMBL, #AB000016;
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InterPro; IPR001553; AAA_ATPase.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1.
Fam; FF01057; AAA, 1.
SMART; SM00382; AAA, 1.
SEQUENCE 668 AA; 76743 MW; 84A210104D9D5788 CRC64;
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Search completed: May 28, 2004, 13:00:04 Job time: 33 secs

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APPLICANT: OTANI, KENICHI
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENITION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307
CURRENT FILING DATE: 1999-10-21
EARLIER PILING DATE: 1999-10-21
EARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET: 2.0
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SEQ ID NOS: 30
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CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
BARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                       Sequence 10, Application US/09422869 Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09422869
Patent No. 6235481
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APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 513
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                    APPLICANT: ODA, NACHISA
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
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US-09-422-869-10
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Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

RIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
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Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-09-12
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EARLIER FILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 40.3%;
1 Similarity 52.4%;
11; Conservative
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Best Local Similarity 61.1%;
Matches 11; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-09-252-991A-17004
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APPLICANT: HORINAMA, YUKIO
APPLICANT: HORINAMA, YUKIO
APPLICANT: HORINAMA, YUKIO
APPLICANT: ODA, NACHISA
APPLICANT: ODA, NACHISA
APPLICANT: ODA, NACHISA
APPLICANT: SEENAN, SEAMUS
APPLICANT: HOU, YUN-PING
APPLICANT: HANIS, CRAIG L.
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAENE I.
ITILE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENT VET.
TEMPORATION OF TYPE
SEC ID NOS: 30
SOFTWARE: PATENT OF TYPE
TEMPORATION NUMBER: 1000-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 544;
66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ODA, NACHISA
APPLICANT: ODA, NACHISA
APPLICANT: SREENAN, SEAMUS
APPLICANT: SREENAN, SEAMUS
APPLICANT: APOLY YUN-PING
APPLICANT: OTANI, KENICH
APPLICANT: HANIS, CRAIG L.
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:3107
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Pred. No. 83;
2; Mismatches
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Pred. No. (
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CURRENT FILING DATE: 1999-10-21
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 672
                        Application US/09422869
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Patent No. 6235481
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Best Local Similarity 47.1%;
Matches 8; Conservative
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ilarity 47.1%;
Conservative
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Best Local Similarity
Matches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
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| Sequence 2, Application US/09794960
| Patent No. 6620592
| GRNERAL INFORMATION:
| APPLICANT: Kapeller-Libermann, Rosana
| TITLE OF INVENTION: 18036, A No. 6620592el Calpain-Like Protease
| TITLE OF INVENTION: and Uses Thereof
| FILE REFERENCE: 35800/209290
| CURRENT APPLICATION NUMBER: US/09/794,960
| CURRENT APPLICATION NUMBER: US/09/794,960
| PRIOR APPLICATION NUMBER: US/09/794,960
| PRIOR APPLICATION NUMBER: US/09/794,960
| PRIOR PILING DATE: 2000-02-28
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: ODA, NACHISA
APPLICANT: ODA, NACHISA
APPLICANT: ODA, NACHISA
APPLICANT: CANATI SERMIS
APPLICANT: SREENAN, SEAMUS
APPLICANT: THOU, YUN-PING
APPLICANT: CHAIL, KENICHI
APPLICANT: HELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
APPLICANT: HIS, CANIC I.
APPLICANT: BELL, GRAEME I.
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 6
LENGTH: 517
TYPE: RT.
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Pred. No. 63;
2; Mismatches 7; Indels
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                                                                                                                                                                Sequence 6, Application US/09422869
                             222 CCVLSPRAGARELGEFH 238
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2 CCVLNRQGGKRNAVLFH 18
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Best Local Similarity 47.1
Matches 8; Conservative
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US-09-794-960-2
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US-09-422-869-6
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US-09-794-960-2
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US COSTOR APPLICATION US/09252991A

1 Sequence 28671, Application US/09252991A

2 Sequence 28671, Application US/09252991A

3 Sequence 28671, Application US/09252991A

3 Patent No. 6551795

4 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

5 TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

5 TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

6 CURRENT APPLICATION NUMBER: US/09/252,991A

7 CURRENT FILING DATE: 1998-02-18

7 PRIOR APPLICATION NUMBER: US 60/094,190

7 PRIOR APPLICATION NUMBER: US 60/094,190

7 PRIOR PILING DATE: 1998-07-27

8 NUMBER OF SEQ ID NOS: 33142

8 SEQ ID NO 28671

8 LENGTH: 276
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Pred. No. 46;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2; Length 232;
Pred. No. 39;
                                                                            COMPUTER REALIZED FORM GISK
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURENT OF STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING APPLICATION: 435
PRIOR APPLICATION NUMBER: US/08/234,440
FILING APPLICATION NUMBER: 10 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGRNT INFORMATION:
NAME: COTUZZÍ, LBULRA A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683-054
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | :: | | | : | | | 156 VCHVRNKRAGKEEPVVVH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ICCVLNRQGGKRNAVLFH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.2%;
Best Local Similarity 38.9%;
Matches 7; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.2%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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MOLECULE TYPE: protein
                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
             RY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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TELEX: 6
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                          Sequence 12444, Application US/09489039A
Sequence 12444, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PELING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR SEQ ID NOS: 14342
SEQ ID NO 12444
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8212
LENGTH: 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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Patent No. 5831009
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Niels P.H.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.1%; Score 43; DB 4;
Best Local Similarity 52.9%; Pred. No. 88;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.6%; Score 42.5; 62.5%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8212, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8212
                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 CSSLSRSGGRRSA--FH 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CCVLNRQGGKRNAVLFH 18
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46 ILNRVGGKENIVSLVH 61
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Best Local Similarity
Matches 10; Conserv
RESULT 9
US-09-489-039A-12444
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US-09-489-039A-8212
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US-08-446-345-38
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APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: With Huter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLBIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                    Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  Score 42; DB 4;
Pred. No. 1e+02;
0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23996 LENGTH: 572 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/906,769
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 99, Application US/08906769
Patent No. 6077687
GENERAL INFORMATION:
                                                                                                                                 ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23996
                                                                                                                                                                                                                                                                                                                                     242 VLRROAGGRRADLRHHP 258
                                                                                                                                                                                                                                                                                            4 VLNROGGKRNAVLFHGP 20
                                                                                                                                                                                                  Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acide
TYPE: amino acide
TOPOLOGY: 14-5
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CCVLNRQGGKRNAV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-906-769-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                08-906-769-99
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                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                        APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
CORRESPONDBNCE ADDRESSE
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-23996
; Sequence 23996, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                   ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPATING SYSTEM: «Unknown»
                                           ; Sequence 5318, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (781)893-5007
TELEPRA: (781)893-8277
INFORMATION FOR SEQ ID NO: 5318:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 384 amino acids
                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 NGGĞĞARDGVTFHG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 NRQGGKRNAVLFHG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                     CITY: Waltham
                         US-09-107-532A-5318
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4 CCPTSRERGNRNRV 17

Search completed: May 28, 2004, 13:02:04 Job time : 14.5 secs Sequence 29, Sequence 29, Sequence 29, Sequence 29, Sequence 25, A

Sequence 31,

Sequence 29, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 31, Appl Sequence 31, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 244, Appl Sequence 244, Appl Sequence 244, Appl Sequence 246, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl Sequence 286, Appl

Sequence 39, Appl Sequence 39, Appl

Perfect score:

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Sequence:

Scoring table:

Database

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Sequence 200078, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)8/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_22697C.1.pep
US-10-424-599-200078
                 US-09-792-630-29
US-09-51-29
US-10-082-671-29
US-10-082-671-29
US-09-792-630-29
US-09-792-630-29
US-09-792-630-29
US-09-792-630-27
US-09-953-351-25
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US-09-953-351-25
US-09-953-351-25
US-10-080-376-27
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US-10-093-100-25
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44.2%; Score 50; DB:
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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Sequence 130, Application US/10317832
Publication No. US20030186337A1
GENERAL INFORMATION:
APPLICANT: Jean-Philippe Girard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |::| ||| |:| |
24 IFNORGNKRNTVIFDG 39
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TYPE: PRT
ORGANISM: Glycine max
                      US-10-424-599-200078
  Sequence 102, App
Sequence 6, Appli
Sequence 120, App
Sequence 9422, App
Sequence 9422, App
Sequence 9423, App
Sequence 9424, App
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Sequence 31, Appl
Sequence 31, Appl
Sequence 37, Appl
Sequence 31, Appl
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Sequence 25, Appl
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                                                                                                                                                                                               (without alignments)
160.719 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/NEG_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
                                                                                                                                                                        May 28, 2004, 12:57:09 ; Search time 34.75 Seconds
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-317-832-130
US-10-317-832-130
US-10-317-832-102
US-10-317-832-102
US-10-188-186-122
US-10-138-977-9422
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US-10-080-376-31
US-10-082-671-37
US-10-097-100-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    1 ICCVLNRQGGKRNAVLFHGP 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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THAP1 AND PAR4 PATHWAYS IN APOPTOSIS CONTROL
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US-10-317-832-6
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Sequence 25, Application US/10317832

Sequence 25, Application US/10317832

Sequence 25, Application US/10317832

Sequence 25, Application US/10317832

APPLICANT: Jean-Philippe Girard

APPLICANT: Sophia Kousaigne

APPLICANT: Francoi Remairic

APPLICANT: Thomas Clouaire

TITLE OF INVENTION: THAPL DEATH ASSOCIATED PROTEINS, AND

TITLE OF INVENTION: THAPL AND PAR4 PATHWAYS IN APOPTOSIS CONTROL

FILE REFERENCE: BIOBANK.009A

CURRENT APPLICATION NUMBER: US/10/317,832

CURRENT PILING DATE: 2002-12-10

PRIOR FILING DATE: 2001-12-18
                                             APPLICANT: SOFILE ACSSIGNA
APPLICANT: Thomas Clouaire
TITLE OF INVENTION: NOVEL DEATH ASSOCIATED PROTEINS, AND
TITLE OF INVENTION: TRAPE AND PAR4 PATHWAYS IN APOPTOSIS CONTROL
FILE REFERENCE: BIOBANK. 009A
CURRENT APPLICATION NUMBER: US/10/317, 832
CURRENT FILING DATE: 2002-12-10
PRIOR PILING DATE: 2002-12-10
PRIOR PLING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FREISEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
43.8%; Score 49.5; DB 14; Length 90;
Best Local Similarity 52.2%; Pred. No. 4.1;
Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Myriam Roussigne
APPLICANT: Myriam Roussigne
APPLICANT: Sophia Kossida
APPLICANT: Francoi Amalric
APPLICANT: Francoi Amalric
APPLICANT: Thomas Clouaire
ITLE OF INVENTION: NOVEL DEATH ASSOCIATED PROTEINS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 95
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Publication No. US20030186337A1
GENERAL INFORMATION:
     Myriam Roussigne
Sophia Kossida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Mus musculus US-10-317-832-25
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-317-832-130
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LENGTH: 90
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Gaps
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APPLICANT: Sophia Kossida
APPLICANT: Sophia Kossida
APPLICANT: Sophia Kossida
APPLICANT: Prancols Amalric
APPLICANT: Thomas Clousiar
TITLE OF INVENTION: NOVEL DEATH ASSOCIATED PROTEINS, AND
TITLE OF INVENTION: THAPL AND PAR4 PATHWAYS IN APOPTOSIS CONTROL
TITLE OF INVENTION: THAPL AND PAR4 PATHWAYS IN APOPTOSIS
CURRENT APPLICATION NUMBER: US/10/317,832
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/341,997
PRIOR RELING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 263
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 577
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-397.

CURRENT APPLICATION NUMBER: US/10/188,186

CURRENT FILING DATE: 2002-07-02

PRIOR APPLICATION NUMBER: 60/303046

PRIOR APPLICATION NUMBER: 60/303046

PRIOR PILING DATE: 2001-07-05

PRIOR FILING DATE: 2003-0303828

PRIOR FILING DATE: 2001-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                  Score 49.5; DE
Pred. No. 9.5;
2; Mismatches
FILE REFERENCE: BIOBANK. 009A
CURRENT APPLICATION NUMBER: US/10/317,832
CURRENT FILING DATE: 2002-12-10
FRIOR APPLICATION NUMBER: 60/341,997
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102
LENGTH: 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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43.8%; Score 49.5;
Best Local Similarity 52.2%; Pred. No. 28
Matches 12; Conservative 2; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10317832
Publication No. US20030186337A1
GENERAL INFORMATION:
APPLICANT: Jean-Philippe Girard
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Best Local Similarity 52.2%;
Matches 12; Conservative
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Gaps

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Sequence 9422, Application US/10335977
Sequence 9422, Application US/20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 280;
               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
PILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANGAGOLEAB, AMW E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...280
SEQUENCE DESCRIPTION: SEQ ID NO: 9422:
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OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9423, Application US/10335977
Publication No. US20040052799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 9422:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 CVLNRQGTRHNNYL 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
         7; Conservative
                                                                  2 CCVLNRQGGKRNAVL
                                                                                                                        143 CCIINNSNGNRTIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                        US-10-335-977-9422
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            Matches
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| Publication No. US20040029789A1
| GENERAL INFORMATION:
| APPLICAMY: Anderson et al.
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
| TILE SERERNEE: 21402-397C
| CURRENT FILING DATE: 2002-07-02
| PRIOR PEDLICATION NUMBER: 60/30346
| PRIOR PEDLICATION NUMBER: 60/30346
| PRIOR PELLING DATE: 2001-07-02
| PRIOR PELLING DATE: 2001-07-03
| PRIOR APPLICATION NUMBER: 60/30318
| PRIOR APPLICATION NUMBER: 60/30318
| PRIOR PELLING DATE: 2001-09-07
| PRIOR PELLING DATE: 2001-09-07
| PRIOR PELLING DATE: 2001-09-07
| PRIOR PELLING DATE: 2001-09-07
| PRIOR PELLING DATE: 2001-09-07
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| PRIOR PELLING DATE: 2001-07-09
| PRIOR PELLING DATE: 2001-07-09
| PRIOR PELLING DATE: 2001-07-09
| PRIOR PELLING DATE: 2001-07-01
| PRIOR PELLING DATE: 2001-07-01
| PRIOR PELLING DATE: 2001-07-01
| PRIOR PELLING DATE: 2001-07-01
| PRIOR PELLING DATE: 2001-07-03
| PRIOR PELLING DATE: 2001-07-03
| PRIOR PELLING DATE: 2001-07-03
| PRIOR PELLING DATE: 2001-07-04
| PRIOR PELLING DATE: 2001-07-04
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    See File Wrapper or PALM.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 12; Length 343; Pred. No. 40;
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR PLILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR PLILING DATE: 2001-07-09
PRIOR PLILING DATE: 2001-07-09
PRIOR PLILING DATE: 2001-07-11
PRIOR PLILING DATE: 2001-07-11
PRIOR PLILING DATE: 2001-07-13
PRIOR PELICATION NUMBER: 60/305262
PRIOR PELICATION NUMBER: 60/305673
PRIOR PLILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
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ORGANISM: Homo sapiens
US-10-188-186-120
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ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Custom
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US-10-188-186-122
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LENGTH: 343
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Gaps

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APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
FILIS REFERENCE: A-70295/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/792,630
CURRENT APPLICATION NUMBER: US/09/792,630
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARR: Patentin version 3.1
SEQ ID NO 31
LENGTH: 461
TYPE: FRT
ORGANISM: goose parvovirus
US-09-792-630-31
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Pred. No. 52;
1; Mismatches 4
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Pred. No. 78;
5; Mismatches
SOFTWARE: UNIX

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANGES MANGES, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
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TELEPHONE: (617)27-7400
TELEPHONE: (617)27-7400
TELEPHONE: (617)27-7400
TELEPHONE: (617)27-7400
TELEMETH: 309 amino acide
TYPE: AMINO ACIDE
TYPE: AMINO ACIDE
TYPE: AMINO ACIDE
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in NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...309
;
SEQUENCE DESCRIPTION: SEQ ID NO: 9424:
US-10-335-977-9424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/09792630 Patent No. US20020168640A1 GENERAL INFORMATION:
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; Sequence 31, Application US/09953351
; Publication No. US20030036643A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 LCGWVKREFNKRNAIWLYGP 171
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, APPLICANT: Melander, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
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Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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US-09-792-630-31
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
IITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
DIAGNOSTICS AND THERAPPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.7%; Score 46; DB 12; Length 299;
64.3%; Pred. No. 50;
tive 1; Mismatches 4; Indels
              RELATING TO HELICOBACTER PYLORI FOR
                                     DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

PILLING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

FILLING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REFERENCE/DOCKET NUMBER: 35,207

TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...299
; SEQUENCE DESCRIPTION: SEQ ID NO: 9423:
US-10-335-977-9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109-1875
COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 9423: SEQUENCE CHARACTERISTICS:
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                                                           NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
                                                                                                                                                                                     STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.3
Matches 9; Conservative
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APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Jin, Cheng He
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FUSION L)
FILE REFERENCE: A-70814/RFY/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/953,351
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
LENGTH: 461
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Pred. No. 78;
5; Mismatches 7; Indel8
                                                                                            Score 46; DB 14; Length 461;
Pred. No. 78;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 28, 2004, 13:04:36
Job time : 35.75 secs
                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/10097100; Publication No. US20030068649A1; GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Melander, Christian
                                                                                                                                                                                                                         152 LCGWVKREFNKRNAIWLYGP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ICCVLNRQGGKRNAVLFHGP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative 5
                                                                                               Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
    ; TYPE: PRT
; ORGANISM: goose parvovirus
US-10-082-671-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: goose parvovirus US-10-097-100-31
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US-10-097-100-31
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APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Jin, Cheng He
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FUSION
FILLE REPERENCE: A-70814/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/953,351
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/232,960
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
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Publication No. US20020172968A1

GENERAL INFORMATION:

APPLICANT: Li, Min

APPLICANT: Dahiyat, Bassil I.

TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES

TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES

TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES

CURRENT APPLICATION NUMBER: US 09/7020 08/706

PRIOR PILING DATE: 2000-02-19

PRIOR PILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.1

SEQ ID NO 31

LENGTH: 461
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Publication No. US20030049647A1
GENERAL INFORMATION:
APPLICANT: DAHIXTH, BASSIL
TITLE OF INVENTION: USE OF NUCLEIC ACID LIBRARIES TO CREATE TOXICOLOGICAL
TITLE OF INVENTION: PROFILES
FILE REFERENCE: XEN/001
CURRENT APPLICATION NUMBER: US/10/082,671
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/270,781
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 58
SOFFWARE: Patentin Ver. 2.1
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PAT 30-MAY-2001		Parvovirus.	ntlichen Rechts
linear		Parvovirinae,	ung des Oeffe
60 bp DNA		Parvoviridae, F e,J.	21-FEB-2001; szentrum Stiftu
AX137750 60 bp Sequence 15 from Patent EP1077260. AX137750	AX137750.1 GI:14273923 Mice minute virus	mice minute Vitus Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus. 1 Nueesch.J. and Rommelaere.J.	Parvovirus ns1 variants Patent: EP 1077260-A 15 21-FEB-2001; Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
RESULT 1 AX137750 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE	OKGANISM REFERENCE AUTHORS	TITLE JOURNAL

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RMLNI HI THTL PGDFGLVDKNEWPM I CAWL VRNGY QSTWAS Y CAKWGKVPDWSENWAE
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Patent: EP 1077260-A 4 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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Patent: EP 1077260-A 1 21-FEB-2001;
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Seguence 1 from Patent BP1077260.
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Matches 59; Conservative
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NTVLFHGPASTGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQ
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Patent: EP 1077260-A 16 21-FEB-2001;
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Mice minute virus
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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/db xref="Ril1427394"

/db xref="Ril1427394"

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                        Location/Qualifiers
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AUTHORS
TITLE
JOURNAL
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AX137747
LOCUS
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HOU34255
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TSPPRDGGYFLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETYETYTTAQETKRGRI
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QVNQFKAICSGQTIRIDQKGKGSKQIEPTVIMTNENITVVRIGGERPEHTQPIRD
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TSPPROGGYFLSSDSGMKTNFLKGEREHLUSKKYTDDNREPSTVETTVTAGETKGRRI
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OVNOFKAICSGOTTI LOOKGKGSKOLEPTYMYNDPPROTOKNYNIKOPINOPING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMLNIHLTHTLEGDFGLVDKNEWPMICAWLVKNGYQSTWASYCAKWGKVPDWSENWAE
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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Patent: EP 1077260-A 8 21-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
(DE)
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                                                                                                                                                           'note="unnamed protein product"
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                                                                             /note="Parvovirus NS1 variant"
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    2019
    /organism="Mice minute virus"
/mol_type="unassigned DNA"
/db_xref="taxon:10794"

/mol_type="unassigned DNA"
/db_xref="taxon:10794"
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/db_xref="REMTREMBL:CAC39
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Sequence 8 from Patent EP1077260.
AX137743
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Best Local Similarity 98.3°
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Mice minute virus
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AX137743
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ARTKTAPDLI LEKAETSKLTNPSLPDTRTCR I FAFHGWNYVKVCHAI CCVLNRQGGKR
NAVLFHGPASTGKS I I AQAI AQAGNVGCYNAANVNFPFNDCTNKNL I WVEEAGNFGQ
QYNQFKAI I CSOQTI R I DQXGKGSKQI BPTPVI MTTNBNI TYVRI GCEBR PEHTQPIRD
RMLNIH LTHTLBGDFGLVDKNEWPWI CAMLVKNGYQSTWASYCAKWGKVDDWSENWAE
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NTKNIFPGDVNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
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TSPPRDGGYPLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGR I
QTKKEVS I KTTLKELVHKRVTSPEDWMMQPDSY I EMMAQPGGENLLKNTLEI CTLTL
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Hamster parvovirus
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
1 (Dases 1 to 4773)
Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Mice minute virus
Mice minute virus
Viruses; BSDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACACCA
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Score 58.4; DB 6; Length 2019;
Pred. No. 6.2e-09;
0; Mismatches 1; Indels 0
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/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                               DNA
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1077260-A 12 21-FEB-2001;
                                                                                                                                                                                                                                                                                     Sequence 12 from Patent EP1077260.
AX137747
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        97.3%;
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Best Local Similarity 98.3
Matches 59; Conservative
          Query Match
Best Local Similarity 98.3
Matches 59; Conservative
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SRAGKKTRPPAYIFINGARAKKKLTSSAAQGSSQTMSDGTSQPDSGNAVHSAARVERA
ADGPGGSGGGGGGGVGVSTGSYDNQTHYRPLGDGWVEITALATRLVHLNNPKSENY
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TLLRTGDEFATGTY YFDTNSVKLTHTWQTNRQLGQPPLLSTFPRADTDAGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVRYSYGKQHGENNASHGPAFERYTÑDETSFGSGRDTKDGFIQSAPLVVPPPLNGILT
NANPIGTKNDIHFSNVFNSYGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFV
CKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGGFFWKGKLTMRAKLRANTTWNPV
YQVSAEDNGNSYMSVTKWLPTATGNWQSVPLITRPVARNTY"
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/note="unnamed protein product; Protein sequence is in
conflict with the conceptual translation; coding sequence"
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The complete DNA sequence of minute virus of mice, an autonomous
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1 (bases 1 to 5149)
                                                                                                                                                                                                                     2332. .2361
/note="unnamed protein product; coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                           2354. .2398
/note="unnamed protein product; coding sequence"
                            1286. .2354
note="unnamed protein product; coding sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
CACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
                                                                                                                                                                     'db_xref="SWISS-PROT:P03137"
'translation="MAPPAKRAKRGKGLRDGWLVGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58.4; DB 14;
Pred. No. 6.4e-09;
0; Mismatches 1;
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Mucleic Acids Res. 11 (4), 999-1018 (1983)
83143341
6298737
                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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translation="MVGWWGINV"
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/db_xref="GOA:P03137"
                                                                                                                                                                                                                                                                      codon start=1
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                                                                                                                                                                                                                                                                                                                      'db_xref="GI:584078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonstructural protein.
Mice minute virus
Mice minute virus
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Best Local Similarity 98.3%;
Matches 59; Conservative
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MVMPCG
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Minute virus of mice with two major open reading frames (genome).
V01115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unnamed protein product; coding sequence"
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/db_xref="G0312"
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SNQLTWAGNAYSDEVLGATNWLKEKSNOEVFSFVFKNENVQLNGKDIGWNSYKKELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGTIKIDOKCKGSKOIEPTPVIMTTNENITVVRIGCEERPEHTOPIRPRALNIHLTH
TLPGDFGLVDKNEWPMICAWLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINL
LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELKSLORGAETTWDOSEDMEWETTVDEMTKKQVFIFDSLVKKCLFEVLNTKNIFPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The messenger RNA of this virus (colinear with the strand listed) is spliced, but the exact splice sites are not known. The listed strand is complementary to the one which is included in the virion. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1502 GGTCBAACTATTCGCATTGATCBAAAGGBAAAGGCAGCAAACAGATTGAACCAACACACA 1561
                         Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996) 96201434
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The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coat protein; genome; origin of replication; overlapping genes; terminal repeat.
Mice minute virus
Mice minute virus
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1 (bases 1 to 5081)
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                                                                                                                                                   Besselsen, D.G.
Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of Veterinary Pathology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 4773;
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Pred. No. 6.4e-09;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                           /organism="Hamster parvovirus"
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/specific_host="Mesocricetus auratus"
/db_xref="taxon:42843"
          and Riley, L.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 11 (4), 999-1018 (1983)
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/mol_type="genomic DNA"
/db_xref="taxon:10794"
          Franklin, C.L., Hook, R.R. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%;
Local Similarity 98.3%;
Les 59; Conservative (
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Matches
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RESULT PAMVM2

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SOURCE

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GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDSGNNVHSAA
RVERAADGPGGSGGGGGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMP
                                                                                                                                                                                                                                                                                                                                                                               NSYKKELQEDELKSLQRGAETTWDQSEDMEWETTVDEMTKKQVFIFDSLYKKCLFEVL
NTRNI FPGDVNWFVQHEWGKDQGWHCHVLIGGKDFSQAQGKWWRRQLNVYWSRWLVTA
CYNQLTPABLAEDNEWVTLLYKHKQTKROTTKCHFGNMI AYYFLTKKKIS
TSPPDGGSPEIKLRE TAEDNEWVTLLYKGKLYTDDMR PETVETVTTAGETKRKIS
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ARTKTAFDLILEKAETSKLTNFSLPDTRTCRIFAFHGWNYVKVCHAICCVLNRQGGKR
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MSQLNLVSLDQEIFNVVLKTVTEQDLGGQAIKIYNNDLTACMMVAVDSNNILPYIPAA
NSMETLGFYPWKPTIASPYRYYFCVDRDLSVTYENQEGTVEHNVMGTPKGMNSQFFTI
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LNGILTNANPIGTKNDIHFSNVFNSYGPLTAFSHPSPVYPQGQIWDKELDLEHKPRLH
ITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVNQFKAICSGQTIRIDQKGKGSKQIEPTPVIMTTNENITVVRIGCEERPEHTQPIRD
MINJHLITHTLBGDFGLVDVDRWPWT CAMLVYKORYQSTWAS YCAKWGKVPDWSERWAE
PKVPTPINLLGSARS PFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
ILPGDFGLVDKNEWPMICAMLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINL
LGSARSPFTTPKSTPLSQNYALTPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
KACQDGQLSPTWSEIEEDLRACFGAEPLKKDFSEPLNLD"
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                                                                                                                                                                                                                                                                                                                                                     translation="MAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGW
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gene="VP"
hote="minor transcription start site"
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                                                                                                                                                                                                                                                             'product="nonstructural protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="alternative intron"
join(2286. 2316,2399. .4557)
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(2286. .2316,2399. .4557)
/gene="VP1"
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                                                                                                                                                                                                                            codon start=1
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/gene="VP"
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/gene="VP"
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                                                                                                                                                                  261. .2279 /
/gene="NS1"
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/gene="VP"
                                                                                                                                     gene="NS1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Minute virus of mice (strain MVM(p)), passed in mouse 1 (variant A-9) cells.

The parvoviridae family cantains two groups that infect mammalian hosts: (i) defective (helper-dependent) adeno-associated viruses, and (ii) autonomous (helper-independent) parvoviruses. MVM is a member of the latter group. Both groups have been demonstrated to package both plus and minus strands (in separate particles) of the sp. DNA genome, though the minus strand is more typically packaged in the latter group.

The sequence below corresponds to the plus (+) strand, also referred to as the C-strand. The minus (-) strand is also referred to as the V-strand.

The 3' and 5' termini both exhibit the potential for forming stable (foll-back) hairpins; these sequences appear to play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replication [1].

The left and right halves of the genome encode two distinct, but overlapping transcriptional units. The transcripts can be summarized [1] (1 map unit (mu) = 51 bp):

R1 (4.8 kb): 4.5 mu - 46 mu; 46+ mu - 95 mu
R2 (3.3 kb): 4.5 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 (3.0 kb): 40 mu - 10.7 mu; 38 mu - 46 mu; 46+ mu - 95 mu
R3 is the major transcript.

There are two major open reading frames, both on the plus (or C) strand. The left side ORF (261-2279) probably encodes a non-capsid protein of 85 kd; the right side ORF probably encodes the viral capsid proteins, VP1 (or A, 83 kd). VP2 (or B, 64 kd), and VP3 (or C, 61 kd). But because of uncertainties about the precise splice points in the transcripts, the exact starts, stops and (possible) intron boundaries are not known.

revision 4804 4870 a-65bp-a in [2]; aa in [1] [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKLREIAEDNEWYTLLTYKHKOTKKDYTKCYLFGNMIAYYFLTKKKISTSPPRDGGY
FLSSDSGWKTNPLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
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SNQLTWAGNAYSDEVLGATNWLKEKSNQEVFSFVFKNENVQLNGKDIGWNSYKKELQE
DELKSLQRGAETTWDQSEDMEWETTVDEMTKKQVFIFDSLVKKCLFEVLNTKNIFPGD
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STGKS I I AQA I AQAVGNVGCYNAANVNFPRNDCTNKNL I WVEBAGNFGQQVNQFKA I C
SGQT I RI DOKGKGSKQ I EPTPV I MTTNENI TVVR I GCEER PEHTQP I RDRMLNI HLTH
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                                                                                                                                                                                                                                                                                       Morgan, W.R. and Ward, D.C.
Three splitcing patterns are used to excise the small intron common
to all minute virus of mice RNAs
J. Virol. 60 (3), 1170-1174 (1986)
      2 (bases 1 to 5149)
Matelly.C.x., darddner, E.M. and Tattersall,P.
DNA sequence of the lymphorropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
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/lab host="mouse 1 (variant A-9) cell"
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/protein_id="AAA67108.1"
/db_xref="GI:825481"
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/strain="MVM(p)"
                                                                                                                                     prototype strain
J. Virol. 57 (2), 656-669 (1986)
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Location/Qualifiers
1. 5149
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/gene="NS1"
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Gaps ;

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/ LTAIN 1 A LOID = "MISSESLDQGAKRWAMFKVYKQMLKSVTYPFFHSVSRDAQKE
SNQLTMAGNAYSDBYLGTTWMLKEKSNQEVFSFVFKTEDVQLAGKDIGWDGWDGWDAGKELQE
BLKSLQGAGTTWDQSEDDMEMESTVDBMTKKQVFTVSLVKKCLFEVLSTKNITAPAD
VTWWYQHEWGCYDGWHTCHVLIGGKDFSQAGSKWWRQLNVYWSRWLYTACNVQLTPAE
RIKLREIAEDSEWYTLLTYKHKQTKKDYTKCVLFGNMIAYYFLTKKKISTSPPRDGGY
                                                                                                                                                                                                                                           MVMICG 5085 bp ss-DNA linear VRL 05-JUL-1995 Minute virus of mice (MVM(i)), a lymphotropic variant of MVM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLSSDSGWKTNFLKEGERHLVSKLYTDDMRPETVETTVTTAQETKRGRIQTKKEVSIK
TTLKELVHKRVTSPEDWMMQPDSYIEMMAQPGGENLLKNTLEICTLTLARTKTAFDL
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STGKSIIAQAIAQAVGNVGCYNAANVNFPFNDCTNKNLIWVEEAGNFGQQVNQFKAIC
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TLPGDFGLVDKNEWPMICAMLVKNGYQSTMASYCAKWGKVPDWSENWAEPKVPTPINS
LGSARSPFTTPKSTPLSQNYAITPLASDLEDLALEPWSTPNTPVAGTAETQNTGEAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses, ssDNA viruses, Parvoviridae, Parvovirinae, Parvovirus. (Dases 1 to 5085)
Astell, C.R., Gardiner, E.M. and Tattersall, P.
DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86115415
Original source text: Minute virus of mice (lymphotropic variant
MVM) DNA, clone pEG222.
Location/Qualifiers
                                                                                                                                                         Length 4761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative splicing; capsid protein; complete genome;
nonstructural protein.
Mice minute virus
Mice minute virus
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                                                             /specific_host="Mesocricetus auratus"
/db_xref="taxon:10794"
                                                                                                                                                     Query Match · 94.7%; Score 56.8; DB 14;
Best Local Similarity 96.7%; Pred. No. 2.2e-08;
Matches 58; Conservative 0; Mismatches 2;
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/codon start=1
/product="nonstructural protein"
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/product="nonstructural_protein"
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/organism="Mice minute virus"
/mol Lype="genomic DNA"
/isolate="lymphotropic variant"
/db xref="texon:10794"
/clone="pEG222"
    minute virus"
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/db_xref="G1:825477"
/organism="Mice minute v
/mol_type="genomic DNA"
/strain="Cutter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prototype strain
J. Virol. 570, 656-669 (1986)
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/gene="NS1"
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/gene="NS1"
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/gene="NS1"
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COMMENT
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MVMICG
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/translation="MSDGTSQPDSGNAVHSAARVERAADGPGGSGGGGGGGGVGVST
GSYDNQTHYRFLGDGWVEITALATRLVHLAMPKSENYCRIRVHNTTDTSVKGNWAKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHEOI WIPWSLVDANAWGVWLOPSDWOYICNTWSQLNLVSLDOBI FNVVLKTYTEQDL
GGOAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
RDLSVTYSNOEGTVEHNVMGTPKGMNSQFFTI ENTQQITLLRTGDEFATGTYYFDTNS
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QVGFCQPHNDPEASRAGPFAAFKVPADITGGVDKEANGSVRYSYGKQHGSNWASHGPA
PERYTWDETSFGSGRDYKDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
GPLTAFSHPSPYYFQGGIWDKELDLEHKPRLHTTAPFVCKNNAFGQMLVRLGPNLTDG
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Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L., Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.
Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Submitted (17-AUG-1995) David G. Besselsen, Department of
Veterinary Pathology, University of Missouri-Columbia, W213
Veterinary Medicine Building, Columbia, MO 65211, USA
1. 4761
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97.3%; Score 58.4; DB 14; Length 5149;
Best Local Similarity 98.3%; Pred. No. 6.4e-09;
Matches 59; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                        /note="ORP2; putative"
/codon start=1
/product="unknown protein"
/protein_id="AAA67113.1"
/db_xref="G1:825484"
/translation="WRNYLFYRPEITWF"
2399. . 4457
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                                                                                                                                                                                product="unknown protein"
                                                                                                                                                                                                /protein_id="AAA67112.1"
/db_xref="G1:825483"
                                                                                                                                                                                                                                    /translation="MVGWWGINV"
2354. .2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAA67114.1"
                                                                   'note="VP intron (alt.)"
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                                                                                                                                   'note="ORF3; putative"
                                                                                                                                                         codon_start=1
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/codon start=1
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Mice minute virus DNA.
                      2317. .2398
/gene="VP"
                                                                                          2332. .2361
/gene="VP"
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/gene="VP1"
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Besselsen, D.G.
                                                                                                                                                                                                                                                                                      gene="VP'
  'number=1
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VERSION
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VERSION
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PAMVMI
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TITLE
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                                                                                         CUVQLTPAERIKLKRĒTAEDSEWVTLLTYKHKOTKKDŸTKCVLFGNMIAYYFLTKKKIS
TSPPROGSTPLSSDSGWKTVELKEGERHLJVSKLYTDDMRDETVETTVTAĞETKEGRI
OTKKEVSIKTTLKELVHKRYTSPEDWMMQDPSYIEMMAQPGGENLLKNTLEICTLTL
ARTKTAFDLILEKAETSKLTNFSLPDTRTCKIPAFHGMNYVKVCHAICCVLNRQGGKR
NYVLEHGRASTGKSIIAADAJAQAVGNVANNUNPPROTOTKNLILWYBRAGNRGQ
OVNOFKAICSGOTIEN DOKGKGSKOJEPTPVINTINRNITVRIGEBRPBHTQDIRD
RMLNIHLTHTDPGDFGLVDKNEWPMICAMLVKNGYQSTMASYCAKWGKVPDWSENWAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKVPTPINSLGSARSPFTTPKSTPLSQNYAITPLAŠDLEDLALEPWSTPNTPVAGTAE
TQNTGEAGSKACQDGQLSPTWSEIEEDLRACFGAEPLKRDFSEPLNLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPP
INTGLILTNAND PIGTKNDI HFSNVFNSYSGPLTARSHSPYVPGOGU WDKREIDLEHKRRLH
ITAPEVCKNNAAPGQULVRLGPNILTDQYDPNGATLSRIYTYGFFWKGKLTMRAKLRAN
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/db_xref="GI:332291"
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                                                       NNYKKELQEDELKSLQRGAETTWDQSEDMEWESTVDEMTKKQVF1YDSLVKKCLFEVL
STKN1APADVTWFVQHEWGKDQGWHCHVL1GGKDFSQAQGKWWRRQLNVYWSRWLVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTQQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTL
TAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPPAAPKVPADVTQGV
                                                                                                                                                                                                                                                                                                                                                                                                             site"
                                                                                                                                                                                                                                                                                                                                     'note="major transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="minor transcription start site"
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                                                                                                                                                                                                                                                                                                                                                                                                             'note="minor transcription start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="alternative intron"
join(2287. 2317,2400. 4558)
/gene="VP1"
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/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown protein"
/protein_id="AAA69568.1"
/db_xref="GI:825478"
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/codon_start=1
/product="unknown_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="alternative intron"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2333. .2362
/gene="VP1"
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/gene="VP1"
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/gene="VP"
                                                                                                                                                                                                                                                           2003. .4558
/gene="VP"
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/gene="VP"
                                                                                                                                                                                                                                                                                                                                                                       1007. .2281
gene="VP"
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/gene="VP"
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/gene="VP1"
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|gene="VP"
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Viruses, SEDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.

1 (bases 1 to 5087)
Sahli,R., McMaster,G.K. and Hirt,B.
DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice
Nucleic Acids Res. 13 (10), 3617-3633 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MSDGTSQPDGGNAVHSAARVERAADGPGGGGGGGGGGGGGVGVST
GSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDD
AHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDĽSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNP
VKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSY
GPLTAFSHPSPVYPQGQIMDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQ
YDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAMVMI : 5087 bp DNA linear VRL 01-JUL-1999
Mouse parvovirus minute virus immunosuppressive variant genome ( =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For the fibroblast-specific strain (MVMp) sequence see <PAMVM2>.

The genomes of MVMp and MVMi (immunosuppressive variant) have more than 96% of their sequence in common.

Data kindly reviewed (18-JUL-1986) by G. McMaster.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACACCA
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Pred. No. 2.2e-08; 0; Mismatches 2;
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/note="terminal hairpin region"
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/organism="Mice minute virus"
                                                                                                                                                                                                                                                                       translation="MFNYLFYRPEITWF"
                                                                                                                                                                                   /product="unknown protein"
/protein id="AAA69571.1"
/db xref="GI:825480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAA69572.1"
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/db_xref="GI:825479"
                                                  translation="MVGWWGINV"
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/db_xref="taxon:10794"
1...116
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                                                                                                                                   'note="ORF2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         start=1
                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                2400. .>4558
/gene="VP1"
                                                                                                                                                                                                                                                                                                                                                                           2795. .4558
/gene="VP2"
2795. .4558
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/gene="VP2"
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Best Local Similarity 96.7%;
Matches 58; Conservative
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SOURCE
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YIYTSAADQRPIDGYKDAKDWGGKVGHYFFRYRARARAKITHOSEPGYSGVSRAGKRY
RPPAYIFINQARAKKLISAAQQSSQTMSGCTSQPDGGNGVHSAARVERAADGPGGG
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DERATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATOM
                                                                                                                                                                                                                                                                                                                                                                                                                                EVNWYSEAIRTRPAQYGFCQPHNDFEASRAGFPAAPKVPADYTGGVDREANGSYRYSY
GKQHGENWAAAGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIG
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GQMLVRLGFNLTDQYDPNGATLSRIVTYGTFFWKGKLTWRAKLRANTTWNPVYQVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQVGFCQPHNDFEASRAGPFAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGP
PERXTWDESTRYBGSGRDTROFEIQSABLVVPPENGILTNAPTGTKONDFESKVFNS
YGPLTAFSHPSPVYPGQQTWDKELDLEHKPRLHITAPPVCKNNAPGQMLVRLGPNLTD
QYDDNGATLSRIVTYGTFFWKGKLTWRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAHEQIWTPWSLVDANAMGVWLQPSDWQYICNTWSQLNLVSLDQEIFNVVLKTVTEQD
SGGQAIKIYNNDLTACMYVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRDLSVTYENQEGTI EHNVMGTPKGMNSQFFTI ENTQQITLLKTGDEFATGTYYFDTN
PVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRL 21-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="TMSDGTSQPDGGNGVHSAARVERAADGPGGSGGGGGGGGGVGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAGATTGAACCAACACCA
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94.7%; Score 56.8; DB 14; Length 5087;

Best Local Similarity 96.7%; Pred. No. 2.2e-08;

Matches 58; Conservative 0; Mismatches 2; Indels 0;
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2792. .4558
/gene="VP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="polyadenylation signal"
4878. .5087
/note="terminal hairpin region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4603. .4608
/note="polyadenylation signal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GOA:P07302"
/db_xref="SWISS-PROT:P07302"
                                                                                                                                                                                                                                                   xref="SWISS-PROT:P07302"
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                     note="TATA box"
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                                                                                                                                                 codon start=1
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                                                                                   <2405. .4558
/gene="VP1"
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Mouse parvovirus 1c

Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

1 (bases 1 to 4764)

Besselsen, D. G., Pintel, D. J., Purdy, G.A., Besch-Williford, C.L.,

Franklin, C.L., Hook, R.R. Jr. and Riley, L.K.

Molecular characterization of newly recognized rodent parvoviruses
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1 (bases 1 to 4764)

Besselsen, D.G., Pintel, D.J., Purdy, G.A., Besch-Williford, C.L., Franklin, C.L., Hook, R.B. Jr. and Riley, L.K.

Molecular characterization of newly recognized rodent parvoviruses J. Gen. Virol. 77 (Pt 5), 899-911 (1996)
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Direct Submission
Submitted (17-AUG-1995) David G. Besselsen, Department of
"-'.....' Missouri-Columbia, W213
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                                                                                                                                                                                                                                                                                                              Veterinary Pathology, University of Missouri-Columbia Veterinary Medicine Building, Columbia, MO 65211, USA Location/Qualifiers
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1 Similarity 95.0%; Pred. No. 7.4e-08;
57; Conservative 0; Mismatches 3;
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Besselsen, D.G.
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RESULT

Mouse parvovirus 1b

U34253.1

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                                  MPU12469 110ear VRL 24-JAN-1995 Mouse parvovirus 1 complete genome, nonstructural protein 1 (NS1) gene, complete cds and capsid protein (VP1) gene, complete cds.
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TRGDRSGITQISGSNDVTEATRVRPAQVGFCQPHDNFETSRAGPFKVPVVPANVTQGN
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NILTNSDBYCOKKTAIHYONVENSYGPLTAFPHPAPIYPOGOJNWKELDLEHKPRLHA
OAPFVCKNNAPGOLLYKLAPHLTDOYDPNSSTLSRIVTYGTFFWKGKLTLKAKLRPNA
TWNPVYQVSAQYQIBNEYMSIHKWLPTATGNMOSIPLLSRPVARNTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MAPPAKRAKRGWVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDE
                                                                                                                                                                                                                                                                                                                                                       Viruges; seDNA viruges; Parvoviridae; Parvovirinae; Parvovirus.

(bases 1 to 5144)

Ball-Goodricht, J. and Johnson, E.

Molecular characterization of a newly recognized mouse parvovirus
J. Virol. 68 (10), 6476-6486 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-UUL-1994) Lisa J. Ball-Goodrich, Section of Comparative Medicine, Yale University School of Medicine, New Haven, CT 06520-8016, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mouse parvovirus 1"
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265. .2283
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Ball-Goodrich, L.J.
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Mouse parvovirus 1
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92.0%; Score 55.2; DB 14; Length 5144; 95.0%; Pred. No. 7.4e-08;

Best Local Similarity

Query Match

ORIGIN

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                     1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACAC
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 Indels
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                                                                          2, 2004, 18:58:37
 57; Conservative
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Job time : 653 secs
 Matches
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2, 2004, 15:24:48; Search time 145.25 Seconds (without alignments) 1754.849 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                June
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1 ggtcaagctattcgcattga.....aacagattgaaccaacac 60 US-10-069-056-15 60 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries N_Geneseq_29Jan04:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2001bs:* geneseqn1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:* geneseqn2004s:*

	Description	Aad02804 Parvoviru	Aad02805 Parvoviru	Aad02801 Parvoviru	Aad02803 Parvoviru	Aad02797 Parvoviru	Aad02799 Parvoviru	Aan40252 Sequence	Aat15311 Non-atten	Aat15312 Attenuate	Aat88321 Attenuate	Aat88324 Attenuate	Aat88320 Canine pa	Aaf22299 BAC conta	Aaf22285 BAC conta	Aaf22282 BAC conta	Continuation (6 of	Abq68065 Listeria	Abq69966 Listeria	Continuation (12 o	Aav26084 Tomato pe	Abl15067 Drosophil
SUMMARIES	ΩI	AAD02804	AAD02805	AAD02801	AAD02803	AAD02797	AAD02799	AAN40252	AAT15311	AAT15312	AAT88321	AAT88324	AAT88320	AAF22299	AAF22285	AAF22282	AAF22303 5	ABQ68065_	ABQ69966	ABA03041 11	AAV26084	ABL15067
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d	Query Match	100.0	100.0	97.3	97.3	97.3	97.3	74.3	70.7	70.7	70.7	70.7	70.7	45.3	45.3	45.3	45.3	44.0	44.0	44.0	43.0	42.7
	Score	09	9	58.4	58.4	58.4	58.4	44.6	42.4	42.4	42.4	42.4	42.4	27.2	27.2	27.2	27.2	26.4	26.4	26.4	25.8	25.6
i	Result No.	н	7	m	4	S	9	7	80	6	10	11	12	c 13	c 14	15	c 16	17	18	c 19	20	21

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Ab118508	Adb07799	Adb07801	Aah15778	Aac76412	Abk94959	Aad21290	Continuat	Abx62995	Aah57512	Aba12234	Aax77013	Aax77012	Aa846237	Ach33393	Aaz16901	Aaf18259	Aas84526	Ab103944	Ab119270	Ab119268	Ab110478
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ABL18508	ADB07799	ADB07803	AAH15778	AAC76412	ABK94959	AAD21290	ADB12064	ABX62995	AAH5751	ABA12234	AAX7701	AAX7701	AAS4623	ACH3339	AAZ1690	AAF18255	AAS84526	ABL03944	ABL19270	ABL19268	ABL10478
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6735	2385	2385	2945	4082	5273	10172	110000	3051	3055	306	3666	3667	12790	445	767	2508	2729	13480	13521	15505	29046
42.3	42.0	42.0	42.0	42.0	42.0	42.0	42.0	41.7	41.7	41.0	41.0	41.0	41.0	40.7	40.7	40.7	.40.7	40.7	40.7	40.7	40.7
25.4	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25	25	24.6	24.6	24.6	24.6	24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4
24	25	56	27	28	59	30	31	32	33	34	35	36:	37	38	39	40	41	42	43	4.4	45
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ALIGNMENTS

/*tag= b /note= "This location corresponds to position 1387 of the variant (T463A) DNA shown in AAD02805" NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds. Parvovirus non-structure protein 1 (NS1) variant (T463A) DNA fragment. /*tag= a /product= "Parvovirus NS1 variant (T463A) peptide" /note= "CDS does not include start and stop codon" Location/Qualifiers replace (40, A) AAD02804 standard; DNA; 60 BP. (first entry) /partial 1. .60 /*tag= (revised) 06-AUG-2003 31-MAY-2001 Parvovirus. Synthetic. AAD02804; mutation RESULT 1 Key AAD02804

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. 99EP-00115161. 99EP-00115161 Rommelaere WPI; 2001-212717/22. EP1077260-A1 13-AUG-1999; 13-AUG-1999; 21-FEB-2001. Nueesch J,

Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

P-PSDB; AAY72709.

Abl15066 Drosophil Aah05198 Human cDN

4 ABL15066 4 AAH05198

4365

42.7

25.6 25.4

Gaps

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0; Indels

100.0%; Score 60; DB 5; 100.0%; Pred. No. 2.7e-10; ive 0; Mismatches 0;

(revised)

Length 2019;

9

us-10-069-056-15.rng

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1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAAGGCAGCAACAACAACAACAACAACAA
                      Sequence 2019 BP; 697 A; 389 C; 453 G; 480 T; 0 U; 0 Other;
therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                        AAD02801 standard; DNA; 2019 BP.
                                                                    60; Conservative
                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                    06-AUG-2003
31-MAY-2001
                                                                                                                                                                                               AAD02801;
                                                                    Matches
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SXS
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                                           variant (7463A) DNA fragment. The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as toxins for gene
                                                                                                                                                                                                                                                                                                                                                                               NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                                                                                                                                                                             Gaps
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                                                                                          diseases. The variant DNAs are useful as vectors for gene (Updated on 06-AUG-2003 to correct OS field.)
                                  sequence is a parvovirus non-structure protein 1 (NS1)
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                                                                                                                                                                                                                                                                                                                                                           Parvovirus non-structure protein 1 (NS1) variant (1463A) DNA
                                                                                                                                                  100.0%; Score 60; DB 5; Length 60; 100.0%; Pred. No. 1.5e-10;
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /"tag= a
/product= "NS1 variant (T463A) protein"
replace(1387, A)
/*tag= b
                                                                                                                            Sequence 60 BP; 26 A; 13 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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             Disclosure; Page 27; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 27-30; 41pp; English
                                                                                                                                                                                                                                                                             AAD02805 standard; DNA; 2019
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                                                                                                                                                                         60, Conservative
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P-PSDB; AAY72710.
                                                                                                                                                            Best Local Similarity
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31-MAY-2001
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Synthetic.
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                                                                                                                                                                                                                                                                                                    AAD02805;
                                                                                                     therapy.
                                                                                                                                                    Query Match
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                                                                                                         NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant; ds.
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                                                    Parvovirus non-structure protein 1 (NS1) variant (T363A) DNA
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                                                                                                                                                                                                                                                                                                                                                 /product= "NS1 variant (T363A) protein"
replace(1187, A)
/*tag= b
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1. .2019
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(first entry)
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Best Local Similarity 98.3
Matches 59; Conservative
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P-PSDB; AAY72706.
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Location/Qualifiers
1. .2019
/*trea= a "Parvovirus NS1 protein"
/product= "Parvovirus NS1 protein"

99EP-00115161 99EP-00115161

(revised)
(first entry)

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Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                             Parvovirus non-structure protein 1 (NS1) wild-type DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nueesch J, Rommelaere J;
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P-PSDB; AAY72702.
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31-MAY-2001
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1381 GGTCABACTATTCGCATTGATCABABGGGAAAGGCAGCAACAACAGATTGAACCACCA 1440
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Pred. No. 9.2e-10;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                        Parvovirus non-structure protein 1 (NS1) variant (T394A) DNA.
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1. .2019
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(first entry)
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                                                                                                                                                                                       AAD02803;
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The present sequence is a wild type DNA encoding parvovirus non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytocoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                     1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAGATTGAACCAACACA
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                         97.3%; Score 58.4; DB 5; Length 2019; 98.3%; Pred. No. 9.2e-10; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parvovirus non-structure protein 1 (NS1) variant (S283A) DNA
                                                                                                                                                                                           Sequence 2019 BP; 698 A; 389 C; 452 G; 480 T; 0 U; 0 Other;
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Best Local Similarity 98.33
Matches 59; Conservative
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31-MAY-2001
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1381 GGTCAAACTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACCACAA 1440

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AAD02797 standard; DNA; 2019 BP

RESULT 5
AAD02797
ID AAD0
XX
AC AAD0

AAD02797

1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACACA

Location/Qualifiers

.2019

/*tag=

mutation

EP1077260-A1

21-FEB-2001

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM

Nueesch J, Rommelaere J;

WPI; 2001-212717/22 P-PSDB; AAY72704.

99EP-00115161 99EP-00115161

13-AUG-1999; 13-AUG-1999; Claim 7; Page 11-14; 41pp; English.

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1 GGTCAAGCTATTCGCATTGATCAAAAAGGCAAGCAAAAAAGACAAATTGAACCAACACC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relative to control
disease in animals,
                                                                                                                                                                                                                                      Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                         The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This viral DNA is isolated from a non- attenuated CPV. The DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.7%; Pred. No. 4e-05;
Matches 50; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3524 BP; 1400 A; 719 C; 648 G; 757 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-attenuated canine parvovirus CPV-39 passage 5 DNA
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CPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated CPV strains contg. up to 4 mutation virus - useful as a veterinary vaccine against such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                             Claim 10; Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parrish CR, Gruenberg A, Carmichael LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 21-24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT15311 standard; DNA; 5049
                               84WO-US000063
                                                                83US-00459203,
84US-00567968,
                                                                                                                                                                                         WPI; 1984-201354/32.
P-PSDB; AAP40306, AAP40675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-251556/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9614088-A1.
                                                                                                                   (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-NOV-1995;
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                                19-JAN-1984;
                                                                 19-JAN-1983;
06-JAN-1984;
02-AUG-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT15311;
                                                                                                                                                      Fox GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT15311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a DNA encoding parvovirus non-structure 1 protein (NS1) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACCAAACACCA 60
                                                                                                                                                                                                                                                                                                                                                                                       Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence from the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2019 BP; 698 A; 389 C; 453 G; 479 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein envelope; immunogen; vaccine; antigen; epitope; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                      /*tag= a
/product= "NS1 variant (S283A) protein"
replace(847, A)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parvovirus; NADL-2 virulent strain.
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Gaps

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'*tag= a 'note= "see AAP40306" 2107. .3522 /note= "see AAP40675"

*tag=

WO8402847-A.

Location/Qualifiers

.2073

AAN40252 standard; DNA; 3524 BP

RESULT 7 AAN40252

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(first entry)

(revised)

24-OCT-2003 12-JAN-1992

AAN40252;

parvovirus

Porcine

Key

97.3%; 98.3%;

Local Similarity 98.3 les 59; Conservative

Matches

Query Match

Sequence 5049 BP; 1790 A; 814 C; 1029 G; 1416 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                 1656 GGACAAACAATTAGAATTGATCAAAAAGGAAAGGAAAGTAAGCAAATTGAACCCAACTCCA 1715
                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This viral DNA is isolated from an attenuated CPV. The DNA is preferably derived from vBI440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM3Z or pGEM5Z. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
preferably derived from vB1440. The DNA is cloned into a vector which is used to transfect a host cell. The vector used is preferably pGEM32 or pGEMS2. The host cells to be transfected ar selected from Norden Laboratory feline kidney cells, mink lung cells, Madin-Darby canine kidney cells or canine A72 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parvovirus; dog; vaccine; CPV; myocardial disease; enteric disease; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Attenuated CPV strains contg. up to 4 mutation (s) relative to control virus - useful as a veterinary vaccine against CPV disease in animals, such as wild or domestic dogs.
                                                                                                                                                                                                                                                                                                                           1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACACA
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                   Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                  Length 5049;
                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated canine parvovirus CPV-39 passage 60 DNA
                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                    Score 42.4; DB 2;
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parrish CR, Gruenberg A, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 24-27; 42pp; English.
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81.7%;
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                                                                                                                                                                                                                                                                            49; Conservative
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                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                      (G in passage
                                                                                                                                                                                                                                                                                                                                                                              passage
                                                                                                                                                                                                                                                                                                                                                                                                                    (A in passage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (T in passage
                                      1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAACAGATTGAACCAACACCA
                   Gaps
                                                                                                                                                                                           parvovirus; CPV; attenuation; vaccine; dog; panleukopenia virus; mink enteritis virus; infection; ds.
                    .;
0
 Length 5049;
                                                                                                                                                                                                                                                                                                                                                                             ٤
                                                                                                                                                                                                                                                                                                          /*tag= c
/note= "base 4307 is A in virulent CPV-39
65 attenuated virus)"
4358
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65 attenuated virus)"
4477
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/note= "base 4477 is G in virulent CPV-39
65 attenuated virus)"
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/note= "base 4889 is C in virulent CPV-39
65 attenuated virus)"
                                                                                                                                                                                                                                                                                                                                                                         /note= "base 4358 is C in virulent CPV-39 65 attenuated virus)"
                    Indels
Score 42.4; DB 2;
Pred. No. 0.00023;
0; Mismatches 11;
                                                                                                                                                                                                                                                                  *tag= a
note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                         'note= "VP1/VP2 coding region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gruenberg A;
                                                                                                                                                                       Attenuated canine parvovirus genomic DNA.
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                             AAT88321 standard; DNA; 5049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOUND INC.
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Query Match
Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                   .4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carmichael LE,
                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-008583/01
                                                                                                                                                                                                                           Canine parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9742972-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-1996;
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                                                                                                                                                    21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1997
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                                                                                                                                                                                           Canine
                                                                                         RESULT 10
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A claimed virus from the 65th passage) wild-type CPV-2b (see AAT88320).

C contains all 6 mutations. The DNA from attenuated CPV strains (see also AAT88324) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks which, in turn, can be transfected into cells to generate master stocks which, in turn, can be transfected into cells to generate master stocks cof the virus. The attenuated viruses can be used in dogs as a vaccine to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), providing a long term immune response. (NB. this sequence was created by adaptation of the wild-type CPV-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                molecule encodes an annenuated canine parvovirus (CPV) genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAAGATTGAACCAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
protection against parvovirus and feline pan-leukopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "base 97 is C or T in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine parvovirus, CPV, attenuation, vB1440, vaccine, dog, feline panleukopenia virus, mink enteritis virus, infection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5049 BP; 1788 A; 809 C; 1029 G; 1417 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42.4; DB 2; Length 5049;
Pred. No. 0.00023;
0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "base 4745 is T in CPV-39 (passage 5)"
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/note= "base 4881 is C in CPV-39 (passage 5)"
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/note= "base 59 is G in CPV-39 (passage 5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Attenuated canine parvovirus (vBI440) genomic DNA.
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/note= "NS1/NS2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "VP1/VP2 coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine parvovirus; vBI440 (ATCC VR 2489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT88324 standard; DNA; 5049 BP
                                                                 Claim 1; Page; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286. .4541
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(first entry)
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21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT88324;
                                                                                                              This DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This DNA sequence comprises an attenuated virus genome derived by serial passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate passaging (60 times) of virulent canine parvovirus (CPV) type 2b isolate CC 39 in Nurs feline kidney host cells. The attenuated virus is designated vB1440 (ARCC WR 2489). It contains 4 mutations relative to the sequence (see AAT88320) of the control (5th passage) wild-type CPV-2b. 2 Mutations are within the hairpin formed by the 3' terminal palindrome: the mutation at nucleotide 59 introduces and into a G-C rich region within the tip of the hairpin, disrupting the base palining in one of the 2 small internal candacent to the mismatched bubble (flip-flop) sequence within the cadacent to the mismatched bubble (flip-flop) sequence within the palindrome. The DNA from attenuated CPV trains (see also AAT88321) is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The attenuated viruses can be used in dogs as a vaccine to protect against feline panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant stransfected), providing a long term immune response.

C (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                           Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5049 BP; 1791 A; 812 C; 1029 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42.4; DB 2; Length 5049;
Pred. No. 0.00023;
0; Mismatches 11; Indels 0.
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/note= "VP1/VP2 coding region"
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/note= "NS1/NS2 coding region"
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                                                                                                                                                                                                       Carmichael LE, Gruenberg A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine parvovirus; type 2b isolate 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; Page 34-37; 60pp; English.
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                                                                                                                                        CORR ) CORNELL RES FOUND INC
97WO-US007584.
                                                                  96US-00647655.
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Best Local Similarity 81.7%;
Matches 49; Conservative
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(first entry)
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   06-MAY-1997;
                                                                      15-MAY-1996;
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21-MAY-1998
                                                                                                                                                                                                           Parrish CR,
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Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant son animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,
                                                                                                                                                                                                                           (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the
                                                                                                                                                                                                           a recombinant DNA construct of a plant
                                                                                                                                                                                                                                                                                                                                           Sequence 85680 BP; 27189 A; 16414 C; 15246 G; 26711 T; 0 U; 120 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51915 ATTCCAGTTGATCAGAAAGGAATAAGCAGTAAACACAACTAATCCACA 51868
                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 85680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAACAAGATTGAACCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producing stably inherited michrosomes which can se
construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC containing repeats from centromeres 1-4 #8.
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                  proteins such as hormones, enzymes, inter? cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                           / Match 45.3%; Score 27.2; Local Similarity 72.9%; Pred. No. 44 hes 35; Conservative 0; Mismatcher
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                                                                                                                                                                     Claim 102; Page 763-777; 1449pp; English.
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                   Keith K;
                                                                                                                                                                                                         present invention relates to
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990S-0127409P.
990S-0134770P.
99US-0153584P.
99US-0154603P.
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                   Copenhaver G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                       WPI; 2000-587529/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1999;
01-APR-1999;
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16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-1999
                   Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF22285;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                   This DNA sequence comprises the genome of virulent canine parvovirus type (CPV-2b) isolate 39, obtained after 5 serial passages in NLFK feline kidney host calls. Putther passaging has yielded attendated virus vB1440 (ATCC VR 2489) (See AAT88124) from the 60th passage, and a claimed virus (see AAT88121) derived from the 65th passage, and a claimed virus (see AAT88121) derived from the 65th passage (ATCC 2528). These crespectively contain 4 and 6 mutations in comparison to the virulent 5th passage virus. The DNA from attenuated CPV-2b strains is used for the production of infectious molecular DNA clones, which, in turn, can be transfected into cells to generate master stocks of the virus. The crement of viruses can be used in dogs as a vaccine to protect against cattenuated viruse and mink enteritis virus. The vaccines protect edine panleukopenia virus and mink enteritis virus. The vaccines protect against the currently prevalent CPV-2b type (and all extant strains of types 2 and 2a), and provide a long term immune response. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1656 GGACAAACAATTAGAATTGATCAAAAGGTAAAGGAAGTAAGGAAATTGAACCACCAA 1715
                                                                                                                                                                                                                   Canine parvovirus DNA carrying specific attenuating mutation(s) - used as vaccines for protection against parvovirus and feline pan-leukopenia virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAAAAAGCAGATTGAACCAACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5049 BP; 1789 A; 813 C; 1030 G; 1417 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC containing repeats from centromeres 1-4 #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42.4; DB 2;
Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                    Gruenberg A;
                                                                                                                                                                                                                                                                                                    Example 8; Page 37-40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centromere; michrosome; vector; ds
                                                                                                            (CORR ) CORNELL RES FOUND INC
                                   97WO-US007584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.7%;
81.7%;
                                                                         96US-00647655
                                                                                                                                                  Parrish CR, Carmichael LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.7
Matches 49; Conservative
                                                                                                                                                                                       WPI; 1998-008583/01
                                   06-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95223 BP; 27974 A; 19452 C; 19355 G; 27745 T; 0 U; 697 Other;
                                                                                         Gaps
                             Sequence 94618 BP; 29114 A; 17215 C; 17486 G; 30801 T; 0 U; 2 Other;
                                                                                                                                                 42709 ATTCCTGTTGATCAGAAAGGAATAAGCAGTAAACACAATTAATCCAGA 42662
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                                                          DB 3; Length 94618;
                                                                                                                    10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAACA 57
                                                    Score 27.2; DB 3; Length 9. Pred. No. 45; 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                 BAC containing repeats from centromeres 1-4 #5.
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cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 102; Page 364-385; 1449pp; English
                                                                                                                                                                                                                                                                                                                                                Centromere; michrosome; vector; ds
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99US-0127409P.
99US-0134770P.
99US-0153584P.
99US-0154603P.
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Best Local Similarity 72.9%;
Matches 35; Conservative
                                                         Query Match
Best Local Similarity 72.9%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                       (first entry)
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13-SEP-1999;
17-SEP-1999;
16-DEC-1999;
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01-APR-1999;
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AAF22282
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13; Indels

49476 ATTCCAGTTGATCAGAAAGGAATAAGCAGTAAACACAACTAATCAAGA 49523

2, 2004, 19:08:36

Search completed: June Job time : 148.25 secs

10 ATTCGCATTGATCAAAAGGAAAAGGCAGCAAAACAGATTGAACCAACA

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1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAGCAACAGATTGAACCAACACCA
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ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
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'cgn2_6/ptodata/2/ina/5A_COMB.seq:*
'cgn2_6/ptodata/2/ina/5B_COMB.seq:*
'cgn2_6/ptodata/2/ina/6A_COMB.seq:*
'cgn2_6/ptodata/2/ina/6B_COMB.seq:*
'cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
'cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-947-823-1
US-08-917-913-4
US-08-817-913-6
US-08-817-913-6
US-08-817-913-6
US-08-817-913-6
US-08-817-913-9
US-08-817-913-10
US-08-817-913-12
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US-08-817-913-16
US-08-817-913-17
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US-08-817-913-17
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US-08-817-913-17
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Maximum Match 100%
Listing first 45 summaries
                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Sequence 343, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Gruenberg, Allen
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STATE: New York
STATE: New York
STATE: New York
STATE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.7%; Score 42.4; DB 1; Best Local Similarity 81.7%; Pred. No. 1.5e-05; Matches 49; Conservative 0; Mismatches 11;
US-08-466-248-19

US-09-751-389-3

US-09-257-381-3

US-09-557-881-1

US-09-643-990A-1

US-09-643-990A-1

US-09-56-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-56-171E-343

US-09-26-537-13

US-09-26-537-13

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US-09-26-537-13

US-09-26-537-13

US-09-26-537-13

US-09-26-537-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFRENCE/DOCKET NUMBER: 7937-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08336345
Patent No. 5814510
MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUENCTH: 5049 base pairs
TYPE: nucleic acid
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1656 GGACAAACAATTAGAATTGATCAAAAGGTAAAGGAAGTAAGGAAATTGAACCAACTCCA 1715
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US-08-647-655-1
Sequence 1, Application US/08647655
Sequence 10, 5885585
GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
APPLICANT: Carmichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.7%; Score 42.4; DB 1; Length 5049; 81.7%; Pred. No. 1.5e-05;
                                                                                                                                                                                                                                      APPLICANT: Gruenberg, Allen
APPLICANT: Gramichael, Leland E.
TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 1036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,345
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30753
REFERENCE/DOCKET NUMBER: 7937-(
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                               RESULT 2
US-08-336-345-2
; Sequence 2, Application US/08336345
; Patent No. 5814510
; GENERAL INFORMATION:
APPLICANT: Parrish, Colin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5049 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 81.7
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-336-345-2
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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1656 GGACAAACAATTAGAATTGATCAAAAGGTAAAGGAAGTAAGCAAATTGAACCAACTCCA 1715
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GENERAL INFORMATION:

APPLICANT: Parrish, Colin R.

APPLICANT: Gruenberg, Allen

APPLICANT: Gruenberg, Allen

APPLICANT: Gramichael, Leland E.

TITLE OF INVENTION: Attenuated Canine Parvovirus Vaccine

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSED: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

STATE: New York

STATE: New York

STATE: DOS6-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/647,655

FILING DATE: ON Even Date Herewith

CLASSIFICATION: 435

MAMR: Gordon Jennifor
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/08/647,655
FILING DATE: On Even Date Herewith
ALEASHFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30,753
REFERENCE/DOCKET NUMBER: 7937-008
TELECOMMUTCATION INFORMATION:
TELEFAK: (212) 790-9090
TELEFAK: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42.4; DB 2;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Patent No. 5885585
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gordon, Jennifer
REGISTRATION NUMBER: 30,753
REFERENCE DOCKET NUMBER: 79:
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.7%;
Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 5049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-647-655-1
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0; Mismatches

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36; Conservative
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  Matches
                                                                                                                                                                                                                                                                                                                                                   1656 GGACAAACAATTAGAATTGATCAAAAAGGTAAAGGAAGTAAGCAAATTGAACCAACTCCA 1715
                                                                                                                                                                                                                                                                                                               1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAAACAGATTGAACCAACACCA
                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                              Length 5049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823 FILING DATE: 09-OCT-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                           Score 42.4; DB 2;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williamson, Valerie M.
Kaloshian, Isgouhi
Yaghoobi, Jafar
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECONMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                              70.7%;
81.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) US-08-947-823-1
5049 base pairs
                                                                                                                                                                                                                                               Best Local Similarity 81.7
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                       nucleic acid
                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
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ZIP: 94111-3834
                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                   US-08-647-655-2
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-947-823-1
  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: STATE:
                                                                                                                                                                                                                                Query Match
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DB 3; Length 51952;

Score 25.8; I Pred. No. 13;

43.0%; 67.9%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                               APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
                                            42427 AAGAAATTCCTAGTTGTCAACAAGTTAAAGATAGCATAAAAATTGAAGCAAGA 42479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
5 AAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAGATTGAACCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 2826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2397 GAATGGAAAAAAGAGGAAAAAGCCCCAAACAGATGGAAAAAA 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
FRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.4; DE Fred. No. 20; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: BALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                              Sequence 282, Application US/09023655 Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 73.8%;
Matches 31; Conservative
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APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2826 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLADNOT04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COPERATING SYSTEM:
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY: BLADN
; CLONE: 1317697
US-09-023-655-282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                          JS-09-023-655-282/c
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Gaps
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40.3%; Score 24.2; DB 3; Length 518;
Best Local Similarity 71.1%; Pred. No. 16;
Matches 32; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TTTTGAAATGGATTAAAAGAAAAAAAAAAAAAAAATAAATTGAACC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCE: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Knobbe, Martens, Olson & Bear
F: 620 Newport Center Drive 16th Floor
Newport Beach
                   APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION: 800
RHICK APPLICATION DATE: 800
RHICK APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-UN-1995
APPLICATION NUMBER: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-UNA-1995
APPLICATION NUMBER: GB941286.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08817913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DY
TELECOMMINICATION :
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-817-913-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                        TELEFAX: 714-760-9502
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Lund, Marianne
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
ADRESSEE: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match . 40.3%; Score 24.2; I
Best Local Similarity 71.1%; Pred. No. 16;
Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08817913
Patent No. 6184443
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 514 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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MOLECULE TYPE:
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ZIP: 92660
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ZIP: 92660
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US-08-817-913-5
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0; Gaps
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40.3%; Score 24.2; DB 3; Length 687;
Best Local Similarity 71.1%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 13; Indels
                        174 TTTTGAATTGATTAAAAGAAAAAAAAAAAAATAAATTGAACC 218
9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
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APPLICANT: Dund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kraiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYOU10.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEGN Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-58P-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/8P95/02196
FILING DATE: 06-UN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               Sequence 8, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08817913
Patent No. 6184443
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 714-760-04
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                  40.3%; Score 24.2; DB 3; Length 631; 71.1%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                     118 rrrrgaaarcgarraaaagaaaaaaaaaaaaaraaarrgaacc 162
                                                                                                                                                                                                                                                                                                                            9 TATTCGCATTGATCAAAAGGAAAAGCCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                  0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHORE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTEN DOS
SOFTWARE: FASTESCO VEFEION 1.5
CURRENT APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-UN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08817913; Patent No. 6184443
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 674 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                         Best Local Similarity 71.1
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.3
Best Local Similarity 71.1
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TELEFAX: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-817-913-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-817-913-7
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15-SEP-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Dedersen, Rolf
APPLICANT: Lund
APPLICANT: Okkels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: G20 Newport Center Drive 16th Floor
CITY: Newport Beach
                                            CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-40N-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 10-CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
TELEPHONE: 714-760-9604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.3%; Score 24.2; D.
Best Local Similarity 71.1%; Pred. No. 18;
Matches 32; Conservative 0; Mismatches
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NATA: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIPICATION BATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altenan, Daniel E
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001AP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-817-913-10
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
TYPE: nucleic acid
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FILING DATE: 1: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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40.3%; Score 24.2; DB 3; Length 6
Best Local Similarity 71.1%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08817913
; Patent No. 6184443
; GENERAL INFORMATION:
APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Keelberg, Finn
APPLICANT: Kreelberg, Finn
APPLICANT: Kreelberg, Penn
APPLICANT: Kreelberg, Penn
CORRESPONDENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                    ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU10.001APC
TELECOMMUNICATION INFORMATION:
TELEFHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: ISSED Version 1.5
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION NUMBER: PCT/EP95/02196
APPLICATION NUMBER: GB941286.7
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: GB941286.7
FILING DATE: 21-OCT-1994
ATTORNEY, AGENT INFORMATION:
NAMM: ALCALL THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABLE TABL
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: DNA (genomic)
US-08-817-913-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 base pairs
             NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                            CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Knobbe, M
                                                                                                                                           Newport Beach
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                                                                                                                                                                             STATE: CA_
COUNTRY: U.8
ZIP: 92660
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ZIP: 92660
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                                                                                                                                                                                                             DB 3; Length 855;
                                                                                                                                                                                                                                                                                                                                       342 TTTTGAAATGGATTAAAAAGAAAAAAAAAAAAATAAATTGAACC 386
                                                                                                                                                                                                          Query Match 40.3%; Score 24.2; DB 3; Length 8: Best Local Similarity 71.1%; Pred. No. 18; Matches 32; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                        9 TATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Pedersen, Rolf
APPLICANT: Lund, Marianne
APPLICANT: Okels, Finn
APPLICANT: Kreiberg, Jette
TITLE OF INVENTION: PROMOTER SEQUENCE FROM POTATO
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02196
FILING DATE: 06-UN-1995
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUIO.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,913
FILING DATE: 15-SEP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08817913
Patent No. 6184443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: DNA (genomic) US-08-817-913-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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US-08-817-913-12
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9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACC 53

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346 TTTTGAAATGGATTAAAAAGAAAAAAAAAAAAATTGAACC 390
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Search completed: June 3, 2004, 00:56:31 Job time: 37.75 secs

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Appl

Sequence

Sequence 12298, A Sequence 18682, A Sequence 111, App Sequence 13530, A Sequence 39530, A Sequence 31901, A Sequence 21447, A Sequence 21447, A Sequence 218, App Sequence 282, App Sequence 218, App Sequence 1768, App Sequence 25, Appli

Scoring table:

Searched:

Perfect score:

Sequence:

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Run on:

Minimum DB seq Maximum DB seq

Database

Sequence 1933, App Sequence 203, App Sequence 3, Appli Sequence 32, Appl Sequence 33, Appl

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Score

Result No.

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3 US-10-377-097-66

0 US-09-814-353-6019

0 US-09-814-353-18682

0 US-09-814-353-18682

0 US-09-814-353-1855

0 US-09-814-353-1855

0 US-09-814-353-1855

0 US-09-814-353-1855

0 US-10-02-600-111

3 US-10-242-535A-39530

6 US-10-424-599-134992

1 US-09-925-302-278

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3 US-10-424-394

1 US-10-10-12-1768

6 US-10-311-455-1348

1 US-10-311-455-1348

3 US-10-311-455-1348

1 US-09-898-779-80

6 US-10-311-455-1348

1 US-09-898-779-80

6 US-10-10-10-2604-133

8 US-10-10-10-2604-133

1 US-09-090-6728-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION WHERE: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
LENGTH: 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA; Cordanismenocytogenes-EGD US-10-398-221-878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2779, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 878, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.03
Matches 39; Conservative
                                                  417
2725
3051
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US-10-398-221-2779
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Sequence 1624, Ap
Sequence 32303, A
Sequence 79561, A
Sequence 244545,
Sequence 244546,
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Sequence 78, Appl
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 21932, A
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                                                                                                               2, 2004, 23:14:04; Search time 141 Seconds (without alignments) 1941.275 Million cell updates/sec
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1: /cgn2_6/ptodate/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodate/2/pubpna/PCTT MEW PUB.seq:*
4: /cgn2_6/ptodate/2/pubpna/PCTT MEW PUB.seq:*
5: /cgn2_6/ptodate/2/pubpna/USO6_NEW PUB.seq:*
5: /cgn2_6/ptodate/2/pubpna/USO6_NEW PUB.seq:*
6: /cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodate/2/pubpna/USO8_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USIOR_PUBCOMB.seq:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-398-221-878
US-10-398-221-2779
US-10-358-977-1624
US-10-369-493-32903
US-10-027-632-244545
US-10-027-632-244545
US-10-027-632-244545
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US-09-822-635-3
US-10-377-097-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-822-635-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match
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and applications

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NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...495

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US-10-335-977-1624
FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                APPLICANT: GLASER, PALLIDDE
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
FILE REFERENCE: 2045-US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR FILING DATE: 2001-00-04
PRIOR PLILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
SEQ ID NO 2779
LENGTH: 2451
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 2451;
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Publication No. US20040652799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLOCBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                           Score 26.4; DB 16; Length Pred. No. 58; 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGDe
US-10-398-221-2779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 495 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1624:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 742-4214
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Best Local Similarity 65.0%;
Matches 39; Conservative
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US-10-335-977-1624
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Sequence 79561, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TTTLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

EROGIN NO 79561

LENGTH: 1925
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slacer, Serven C.
APPLICANT: Slacer, Serven C.
APPLICANT: Slacer, Serven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 32293
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                                                    Gaps
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  Length 495;
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     DB 13;
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Pred. No. 1.2e+02;
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US-10-424-599-79561
42.3%; Score 25.4; C 68.6%; Pred. No. 80; Live 0; Mismatches
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Pred. No. 97;
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity 64.4%;
Matches 38; Conservative
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; ORGANISM: Xylella fastidiosa
US-10-369-493-32903
  Query Match
Best Local Similarity 68.6
Matches 35; Conservative
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Best Local Similarity
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US-10-369-493-32903/c
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-244546
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Sequence 244546, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Dolymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT PAPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/18,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PELICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-09-28
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Pred. No. 1e+02;
1; Mismatches 19; Indels 0
21; Indels
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification and Mapping of Single North Title OF INVENTION: Identification and Mapping of Single North Title OF INVENTION: Polymorphisms in the Human Genome TITLE OF INVENTION: Polymorphisms in the Human Genome CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR PRIOR PAPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR PLING DATE: 2000-07-12 PRIOR PLING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-24 PRIOR FILING DATE: 2000-03-24 PRIOR FILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 1999-09-28
Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 64.3%;
Matches 36; Conservative
38; Conservative
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TRNGTH: 624
  Matches
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TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/128,006
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR PELICATION NUMBER: US 60/195,218
PRIOR PELICATION NUMBER: US 60/185,218
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELING DATE: 1099-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 244545
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REPERBUCE: 108827.12
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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Pred. No. 1e+02;
1; Mismatches 19;
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                                                                                                                                                                                                                                                               DB 13;
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 244546
LENGTH: 624
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Sequence 244546
Publication No. US20030204075A9
GENERAL INFORMATION:
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Publication No. US20030204075A9
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Best Local Similarity 64.3%;
Matches 36; Conservative
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42.0%; Score 25.2; DB 9; Length 5273;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 18; Indels 0
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TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELLORTION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR PELLING DATE: 2000-02-24
PRIOR PELLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-10-28
PRIOR PELLING DATE: 1999-02-8
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR PELLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASSES for Windows Version 4.0
SSQ ID NO 244546
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CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 78
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Best Local Similarity 64.3'
Matches 36; Conservative
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Wang, Jian-Rui
Wang, Dunrui
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ORGANISM: Homo sapiens
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; LOCATION: (93)..(4832)
US-09-728-952-78
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; ORGANISM: Human
US-10-027-632-244546
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US-09-728-952-78
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; Sequence 3, Application US/09822635 ; Patent No. US20010039331A1

US-09-822-635-3 ; Sequence 3, Ap

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APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Moyers, Rachel E.
APPLICANT: Moyers, Rachel E.
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APPLICANT: Buddho-Owen, Laura A.
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APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 10448-035001
CURRENT APPLICATION NUMBER: US/09/822,635
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,921
PRIOR PLING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25.2; DB 9; Length 5
Pred. No. 1.8e+02;
0; Mismatches 18; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68
LENGTH: 5430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 68, Application US/10377097
Publication No. US20040033509A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5430
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US-09-814-353-21932
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Publication No. US20030165831A1

GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                1 GGTCAAGCTATTCGCATTGATCAAAAAGGAAAAGGCAGCAAACAGATTGAACCA 54
                                                                                                                                                                                                                                                1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAGATTGAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hunter, John J.
APPLICANT: Hunter, John J.
APPLICANT: Hunter, John J.
TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 10448-035001
CURRENT APPLICATION NUMBER: US/09/822,635
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,921
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                              Query Match 42.0%; Score 25.2; DB 13; Length Best Local Similarity 66.7%; Pred. No. 1.8e+02; Matches 36; Conservative 0; Mismatches 18; Indels
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42.0%; Score 25.2; DB 9;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 36; Conservative 0; Mismatches 18;
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i OTHER INFORMATION: n = A,T,C or G
US-09-822-635-1
                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-822-635-1
Sequence 1, Application US/09822635;
Patent No. US20010039331A1
GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (3667)...(9113)
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM: Homo Sapiens
                       ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5430)
US-10-377-097-68
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LENGTH: 10172
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GENERAL INCOMENTION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Willennium Pharmaceuticals, Inc.
APPLICANT: Willennium Pharmaceuticals, Inc.
APPLICANT: Williamson, Mark W.
APPLICANT: Williamson, Mark W.
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Huneer, John J.
APPLICANT: Radolph-Owen, Laura A.
APPLICANT: Bandaru, Rajasekhar A.
APPLICANT: Bandaru, Rajasekhar A.
APPLICANT: Bandaru, Rajasekhar A.
APPLICANT: Bandaru, Rajasekhar A.
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APPLICANT: Bandaru, Rajasekhar A.
APPLICANT: Bandaru, Rajasekhar A.
APPLICANT: Bandaru, Rajasekhar A.
APPLICANT: Bandaru, Rajasekhar A.
CURRENT FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-01-17
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 60/218,053
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
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NAME/KRY: misc_feature
LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 625, 9644, 9646, 9658, 9667,
LOCATION: 9671, 9674, 9675, 9691, 9696, 9697, 9700, 9715, 9717, 9726,
LOCATION: 9736, 9737, 9738, 9741, 9743, 9754, 9760, 9768, 9771, 9773, DICCATION: 9782, 9780, 9844, 9921, 9939, 10171, 10172
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGTCAAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAACCA
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42.0%; Score 25.2; DB 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 36; Conservative 0; Mismatches 18;
                                  PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSECSEQ FOR Windows Version 4.0
SEQ ID NO 21932
LENGTH: 10172
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PRIOR APPLICATION NUMBER: US 09/892,870
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,174
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/775,117
PRIOR FILING DATE: 2001-02-01
APPLICATION NUMBER: US 60/216,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-377-097-66; Sequence 66, Application US/10377097; Sequence 66, Application US/103509A1; Publication No. US20040033509A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Search completed: June 3, 2004, 03:14:14 Job time: 143 secs

46.0 435 28 AQ292792 46.0 693 29 CE744031 46.0 936 14 CD45995 45.7 818 28 BZ736749 45.3 303 14 CB179134 45.3 78 6 13 BU558940 45.0 322 9 AA389222 44.3 443 13 BY531592	44.3 554 12 BJ34121 44.3 623 12 BJ575778 44.3 790 14 CA234423 .44.3 839 12 BM051362 44.0 288 10 AW531936 44.0 682 28 BZ208471	44.0 720 13 BX646259 43.7 129 28 BH195940 43.7 233 12 BJ360637 43.7 523 28 AQ058397 43.7 568 12 BI617993 43.7 632 28 AZ773787	43.7 662 28 AZ445385 43.7 678 29 CG324046 43.7 945 12 BI248089 43.7 978 29 CNS0058W 43.3 498 10 AW911058	26 43.3 600 28 AZ857090 AZ857090 AZ857090 ZBOUG61P22 26 43.3 716 12 BG789029 BG789029 SEAUMC008 26 43.3 777 28 AZ838766 AZ838766 ZBOU34815 Z6 43.3 777 28 AZ838766 AZ838766 ZBOU34815 Z6 43.3 1008 29 AJ584309 ZBOU364815 Z5.8 43.0 637 29 CE344963 CE344963 CE344963 Ligr-gas-25.8 43.0 725 29 CG324054 CG3134054 CG3134054 Z5.8 43.0 725 29 CG324054 CG3134054 CG3134054 Z5.8 43.0 833 14 CB661347 CB661347 CB661347 OSJURG04A Z5.8 43.0 851 28 BH678428 CG428358 PUHGAF1TB Z5.8 43.0 871 28 CC428358 CC428358 CC428358 PUHGAF3TB Z5.8 43.0 871 28 CC357676 PUHKG36TB	s t 29 to	Bovidae; Bovinae; Bos. 1 (bases 1 to 820) Lin,S., Najar,F.2., Adelson,D., Gill,C.A. and Roe,B.A. Lin,S., Najar,F.2., Adelson,D., Gill,C.A. and Roe,B.A. Bovine BAC End Sequences from Library TAMBT Unpublished (2003) Contact: Bruce A. Roe Advanced Center for Genome Technology University of Oklahoma Department of Chemistry and Biochemistry Copy Sarrington Oval, Room 208, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Class: BAC ends High quality sequence start: 112 High quality sequence stop: 707.
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			, , , , , , , , , , , , , , , , , , ,	RESULT 1 CC908309 LOCUS DEFINITION ACCESSION VERSION XEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: June 2, 2004, 18:15:21; Search time 1499.5 Seconds	(Without alignments) Title: US-10-069-056-15 Perfect score: 60 Sequence: 1 ggtcaagctattcgcattgaaacagattgaaccaacacc 60 Scoring table: IDENTITY_NUC	Gapop 1 1: 2751328 1mber of hits sa DB seq length:		Database: BST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estor:* 10: gb_est:* 11: gb_htc:* 13: gb_est3:* 14: gb_est3:* 14: gb_est4:*		the 1 the 1 the 2 the 2 the 3 the 3 the 3 the 4

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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ilarity 73.5%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 13;
                                  DB 28;
                                                                            16;
                                Score 28.4; DB 28
Pred. No. 5.6e+02;
0; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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    .466
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 42 row: K column: 22
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                           BE751141.1 GI:10165133
                                     47.3%;
70.4%;
                                                        Best Local Similarity 70.4
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (cow)
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Best Local Similarity
Matches 36; Conserv
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                                       Query Match
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ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                           RESULT 3
BE751141/c
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PUBMED
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BJ360453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                                                                                                                                                              d
                                                                                                                                                              /cell_type="Blood"
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/clone_loctor: pBeloBACI1; Site_1: HindIII; Site_2:
HindIII; TAMBI Bovine BAC library (Wale) produced by Texas
A&M University, Department of Animal Science."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ148321
CH230-267G24.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-267G24, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Fleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 267 row; G column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lases 1 to 778)

Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Brain"
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Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                Length 820;
                                                                                                                                                                                                                                                                                                                                                                                                                                        512 GCTATCAGAATATACCAAAAAGGAAAAGACACAAAACAGAATGAA 556
                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other GSSs: CH230-267G24.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                 7 GCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTGAA
                                                                                                                                                                                                                                                                                                                Score 29; DB 29;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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                                       organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ148321.1 GI:23789271
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                                                                                                                                                                                                                                                                                                              / Match 18:3%;
Local Similarity 77.8%;
Les 35; Conservative
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                     Query Match
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Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
90.9809094.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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/clone lib==WhRRC 2BOV"
/clone lib=WhRRC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue From testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
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Length 778;
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BE751141
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Length 435; Indels

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cb/44U31 693 bp DNA linear GSS 30-SEP-2003
tigr-gss-dog-17000330588335 Dog Library Canis familiaris genomic,
genomic survey sequence.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. I (bases 1 to 693)
Kirkness E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
                                                                                                                                                                                         /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                         Query Match 46.0%; Score 27.6; DB 28; Best Local Similarity 67.2%; Pred. No. 9.7e+02; Matches 39; Conservative 0; Mismatches 19;
                                                                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="plate=2195 Col=11 Row=B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"

    435
    organism="Homo sapiens"

                        High quality sequence stop: 435.
Location/Qualifiers
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Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE744031.1 GI:37084378
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Canis familiaris
                                                                                                                                                                                /sex="male"
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    Class: BAC ends
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Matches 33; Conserv
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ292792

HS_2195_B1_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=11 Row=B, genomic survey
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    EST 07-MAR-2002
BJ360453 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc6m05 5', mRNA sequence.
                                                                                                                              Dictyostelium discoideum
Dictyostelium discoideum
Bictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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46.3%; Score 27.8; DB 12; Length 240;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0
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Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                  Unpublished (2002)
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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High Throughput Sequencing Center
University of Washington
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Sequence Tagged Connector
Plate: 2195 row: B column: 11
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/clone="ddc6m05"
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/strain="AX4"
                                                                                      BJ360453.1 GI:19260048
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AQ292792.1 GI:4010585
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CB179134 303 bp mRNA linear EST 31-JAN-2003 io01c10:x1 Kaestner ngn3 wt Mus musculus cDNA 3', mRNA sequence.
CB179134
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce (mscearcemail.med.upenn.edu)
Seq primer: -400P from Gibco
High quality sequence stop: 247.
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Other ESTs: ioOlc10.y1
Other ESTs: ioOlc10.y1
Endocrine Pancres
Endocrine Pancres
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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                                                                                                                                                                                                                                                                                             /db_xref="taxon:4577"
/clone="ZWMBMa0247A20"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBGSK-; Site_1: HinclI; 0.7-1.5 }
methylation filtered genomic_DNA_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 27.4; DB 28; Length 818; 75.6%; Pred. No. 1e+03; 1.ive 0; Mismatches 11; Indels 0
9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 AAGATATGAGCATGAACAAAAAATGCAGCAATCAGCTTG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AAGCTATTCGCATTGATCAAAAGGAAAAGGCAGCAAACAGATTG
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/strain=1129/Sv x CD1"
/db xref="taxon:10090"
/de_stage="p.c. 14.5"
/lab host="E. coli-DH128 (GIBCO)"
/clone_lib="Kaestner ngn3 wt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/strain="B73"
                                                                                                                                                                                           1. .818
/organism="Zea mays"
                                                                                                                                                                Location/Qualifiers
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                                                                                                                  Seg primer: TR
Class: sheared ends.
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Best Local Similarity 75.69
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AUTHORS
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CB179134
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| Jab_host="E. coli DH10B"
|clone_lib="Fg09_AAFC_ECORC_Fusarium_graminearum_simple_su
| bstrate="
                                                                                                                                                                                                                                                                                                      Watson, R.J., Heys, R., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J., Lacroix, C., Masotti, M., Ouellet, T., Robert, L.S.,
Singh, J.A., Sprott, D. and Tinker, N.A.
A cDNA library prepared from Fusarium graminearum grown on a simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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             EST 03-JUN-2003
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             CD459995 103-JUN-2003
Fg09_07g13_A Fg09_AAFC_ECORC_Fusarium_graminearum_simple_substrate
Gibberella_zeae cDNA clone Fg09_07g13, mRNA sequence.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II+; Site I: EccRI; Site 2:
XhoI; Fusarium graminearum grown on a simple substrate-
minimal media supplemented with amino acids."
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                                                                                                                                                                        Gibberella zeae
Gibberella zeae
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Baggo 20, Central Experimental Farm, Ottawa, Ontario, KlA 0C6, CANADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5518"
/clone="Fg09_07g13"
/tissue_type="Mycelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrigagr.gc.ca.
Location/Qualifiers
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Other_GSSs: OGFBP10TC
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ736749.1 GI:28715835
                                                                                                                  CD459995.1 GI:31374735
                                                                                                                                                                                                                                                                             (bases 1 to 936)
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                                                                                               CD459995
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SOURCE ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

BZ736749 RESULT 8

ACCESSION

VERSION KEYWORDS

Matches

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ORIGIN

Query Match

DRIGIN

Matches

ò 셤 DEFINITION

LOCUS

RESULT 10 BU558840

ACCESSION

VERSION KEYWORDS

SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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AA389222 32-APR-1997
mp24AD8.rl Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
clone IMAGE:570207 5' similar to gb:X65488 cds1 HETENGENOUS
NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 32).

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: Sal1; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. 8.5dpc embryos. pCMV-SPORT2 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:570207"
/tissue type="embryo"
/tes stage="8.50pc embryos"
/lab_hose="DH108"
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY531592
BY531592 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630214M15 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                   734 TACTGGGATTTGTNAAAAAAAAAAGGAAAAAAAAAAAGATTTAACCAAAA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 GCTATTCGCATTGATCAAAAGGAAAAGGCAGCAACAGATTGAACCAACA
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  Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
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BY531592.1 GI:26865971
EST.
Mus musculus (house mouse)
Mus musculus
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Mus musculus
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AA389222/c
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Not I; Site 2: Sal I; The library was prepared by Catherine S. Lee and has not been published. The pancreas was obtained from Gerard Gradwoll (PNAS 97 P1607-1611, 2000). The cDNA's were prepared with an oligo containing a NotI site, and Sall linkers were added to the ends. The inserts were cut with NotI before being cloned into the NotI-Sall sites in the vectors. This is one of two libraries, ngn3 wt and ngn3 -/-. The wt library is in pSPORTI, T7 promoter is 5'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:6587429"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC_144"
/note="Organ: Brain; Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc); Site_2: Sfil (ggccattatggcc); Site_2: Sfil (ggccattatggcc); and 3' adaptors were used in cloning as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein
cDNA Library Arrayed by: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2802 row: j column: 05
High quality sequence stop: 593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 786)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 10337658 NIH_MGC_144 Mus musculus cDNA clone
IMAGE:6587429 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                   45.3%; Score 27.2; DB 14; Length 303; 67.9%; Pred. No. 1.3e+03; Live 0; Mismatches 18; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 71.4%;
Matches 35; Conservative (
                                                                                                                                                                                                                                                                                                                                                                              38; Conservative
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; 0 57 EST 14-DEC-2002

ORGANISM

9 TATTCGCATTGATCAAAAGGAAAAGGCAGCAACAACAGATTGAACCAACA 57

ORIGIN

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Email: genome-res@gsc.riken.go.jp, URL:http://genome-res@gsc.riken.go.jp, awa.T., Arakawa.T., Arakawa.T., Arakawa.T., Miyazaki,A., Murata,M., Nakai,K., Matahiki,A., Numazaki,R., Shizaki,Y., Shizaki,Y., Direct Submission Computational Analysis of Full-Length Mouse CDNAs Computation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 167-163 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2001)
                                                                             Ltoh, M., Kagawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Shinagawa, T., Miyazaki, A., Hashizume, W., Imotani, K., Ishii, Y., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length construction of a norcyclopedia: real-time sequence clustering for construction of a noncedundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Expressional and Sequenced in Mouse Genome Construction Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                   (bases 1 to 443)
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TITLE

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tigr-gss-dog-17000332245527 Dog Library Canis familiaris genomic,
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                                                                      /clone="F630214M15"
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/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
                                                                                                                                                                                                                                                                                                                                                                                                BJ341121 Dictyostelium discoideum cDNA linear EST 07-MAR-20
BJ341121 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda5e11 3', mRNA sequence.
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1 (bases 1 to 554)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="mat A"
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Center For Genetic Resource Information
National Institute of Genetics
National Institute of Senetics
TII Yata, Mishims, Shizuoka 411-8540, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Dictyostelium discoideum"
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                                                                                                                                                                                  Score 26.6; DB 13;
Pred. No. 1.8e+03;
0; Mismatches 14;
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organism="Mus musculus"
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                                                      'db_xref="taxon:10090"
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Location/Qualifiers
             /mol_type="mRNA"
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Dictyostelium discoideum
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BJ341121.1 GI:19249483
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GSS.
Canis familiaris (dog)
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Best Local Similarity 71.4%;
Matches 35; Conservative
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Best Local Similarity 76.2
Matches 32; Conservative
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Location/Qualifiers

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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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(bases 1 to 623)
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Unpublished (2002)
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/clone_lib="Ipomoea nil mixture of flower and flower bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ575778 Ipomoea nil mixture of flower and flower bud Ipomoea nil cDNA clone jm31a10 3', mRNA sequence.
BJ575778 BJ575778 BJ575708.1 GI:27257606
                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
I (bases 1 to 621)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
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periphe"cal blood"
                                                                                                                                                         The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Canis familiaris"
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Ipomoea nil
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Search completed: June 3, 2004, 00:54:16 Job time : 1504.5 secs This Page Blank (uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 28, 2004, 12:48:18; Search time 47.5 Seconds (without alignments) 118.967 Million cell updates/sec

US-10-069-056-17

Perfect score:

1 GQAIRIDQKGKGSKQIEPTP 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 29Jan04:* Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:*geneseqp2003bs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

ou	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Parvoviru	Sequence	Adeno ass	Adeno-ass	Adeno ass	Adeno-ass	NS1 prote	Goose par	Goose par	Goose par	NS1 prote	Parvoviru	Goose par	Adeno ass	Adeno-ass	Adeno ass	Adeno-ass	Barbary d	NS1 prote	Muscovy d
Description	Aay72709	Aay72710	Aay72708	Aay72706	Aay72702	Aay72704	Aap40306	Abu97916	Adb70945	Abu97914	Adb70943	Aay97725	Aae22892	Aae28649	Aae26945	Abu64870	Abu64765	Abr43403	Abu97915	Adb70944	Abu97913	Adb70942	Aar85384	Aay97724	Aae22891
ΩI	AAY72709	AAY72710	AAY72708	AAY72706	AAY72702	AAY72704	AAP40306	ABU97916	ADB70945	ABU97914	ADB70943	AAY97725	AAE22892	AAE28649	AAE26945	ABU64870	ABU64765	ABR43403	ABU97915	ADB70944	ABU97913	ADB70942	AAR85384	AAY97724	AAE22891
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Length	20	672	672	672	672	672	690	312	312	397	397	461	461	461	461	461	461	461	536	536	621	621	626	626	626
% Query Match	100.0	100.0	96.1	96.1	96.1	96.1	96.1	69.9	6.69	69.8	69.8	6.69	6.69	69.9	6.69	6.69	6.69	6.69	69.9	6.69	69.9	6.69	6.69	69.9	6.69
Score	103	103	66	66	66	66	66	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72
Result No.		7	m	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aae28648 Muscovy d Aae26944 Muscovy d Abu64869 NS1 prote		Aay97722 Rep prote Aae22889 Barbarie Aae22890 Goose par		Aae26942 Barbarie Abu64868 Rep prote Abu64867 Rep prote	Abu64762 Parvoviru Abu64763 Parvoviru Abr43401 Goose par	
AAE28648 AAE26944 ABU64869	ABU64764 ABR43402 AAY97723	AAY97722 AAE22889 AAE22890	AAE28646 AAE28647 AAE26943	AAE26942 ABU64868 ABU64867	ABU64762 ABU64763 ARR43401	ABR43400 AAY97713
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27 27 27	727	72 72 27	72 72 72	72 72 72	27 27 27	72
26 27 28	29 30 31	332 4432	35 37	38 39 40	4 4 4 1 2 c	444

ALIGNMENTS

NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant. Parvovirus non-structure protein 1 (NS1) variant (T463A) peptide. Location/Qualifiers 3 AAY72709 standard; peptide; 20 AA. (revised)
(first entry) Misc-difference 06-AUG-2003 31-MAY-2001 Parvovirus. Synthetic AAY72709;

/note= "Wild type Thr substituted with Ala; This location corresponds to position 463 of the NS1 variant (T463A) shown in AAY72710" 99EP-00115161. 13-AUG-1999; EP1077260-A1 21-FEB-2001.

Rommelaere J; Nueesch J,

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

99EP-00115161

13-AUG-1999;

WPI; 2001-212717/22. N-PSDB; AAD02804.

Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.

Disclosure; Page 30; 41pp; English.

The present sequence is a peptide fragment of parvovirus non-structure protein 1 (NS1) variant (T463A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the

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672

(revised)
(first entry)

us-10-069-056-17.rag

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NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                Parvovirus non-structure protein 1 (NS1) variant (T394A)
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   461 GQAIRIDQKGKGSKQIEPTP 480
                                                                                                                                                                      AAY72708 standard; protein;
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N-PSDB; AAD02803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parvovirus
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                                                                                                                                                                                                                                             AAY72708;
                                                                                                      RESULT 3
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cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                      100.0%; Score 103; DB 4; Length 20; 100.0%; Pred. No. 7e-10; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parvovirus non-structure protein 1 (NS1) variant (T463A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY72710 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 30-32; 41pp; English
                                                                                                                                                                                                                                                                                                                                                 1 GOAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                           GQAIRIDQKGKGSKQIEPTP 20
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(first entry)
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                          Similarity 100.
20; Conservative
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                                                                                                                                          Sequence 20 AA;
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parvovirus.
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                                                                   therapy.
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/note= "Wild type Thr substituted with Ala"

99EP-00115161.

Rommelaere

Location/Qualifiers

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                                                                                                                                                                                                                                              (T394A). The invention relates to the variants of the parvovirus nonstructure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                    The present sequence is parvovirus non-structure protein 1 (NSI) variant
Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY72706 standard; protein; 672 AA.
                                                                                                                                                  Claim 6; Page 25-27; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 GQTIRIDQKGKGSKQIEPTP 480
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(first entry)
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31-MAY-2001
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Gaps

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GQAIRIDQKGKGSKQIEPTP 20

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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                         Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.1%; Score 99; DB 4; Length 672; 95.0%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parvovirus non-structure protein 1 (NS1) variant (S283A)
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0; Mismatches
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                                                   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
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Les 19; Conservative
                                                                                      Rommelaere J
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N-PSDB; AAD02799.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 672 AA;
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                13-AUG-1999;
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                                                                                      Nueesch J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is parvovirus non-structure protein 1 (NSI) variant (T363A). The invention relates to the variants of the parvovirus nonstructure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotxcicty activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
                                 NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                             /note= "Wild type Thr substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 672;
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non-structure protein 1 (NS1) variant (T363A)
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Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 19-21; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 GQTIRIDQKGKGSKQIEPTP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY72702 standard; protein; 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumoural disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-00115161.
                                                                                                                                                                                                                                                                                     99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.1%;
95.0%;
                                                                                                                                                                                                                                                                                                                        99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Nueesch J, Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-212717/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD02801.
                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1999;
                                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                        13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1077260-A1
                                                                                                                                                                                                                 EP1077260-A1
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31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2001
                                                                                                                                                                                                                                                    21-FEB-2001
                                                                                          Parvovirus.
                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72702;
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RESULT

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Gaps

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Polypeptide production; protein production; target protein;
high throughput directed evolution; rational mutagenesis; AAV;
protein variant generation; virus titering; Adeno associated virus;
                                                                                                                                                              Adeno associated virus (AAV) mutant rep protein #526.
                                                                                     ABU97916 standard; protein; 312 AA.
 1 GOAIRIDOKGKGSKQIEPTP
                        464 GQTIRIDQKGKGSKQIEPTP
                                                                                                                                                                                                                                                                                                                                                          27-AUG-2001; 2001US-0315382P.
17-DEC-2001; 2001US-00022249.
                                                                                                                                                                                                                                                                                                                                   16-AUG-2002; 2002WO-IB003921
                                                                                                                                                                                                                          rep protein; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                              (NAUT-) NAUTILUS BIOTECH
                                                                                                                                                                                                                                                Adeno associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                      Vega M, Drittanti L,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-354538/33.
                                                                                                                                                                                                                                                                                    WO2003023032-A2.
                                                                                                                                     30-JUL-2003
                                                                                                                                                                                                                                                                                                            20-MAR-2003
                                                                                                                                                                                                                                                             Synthetic.
                                                                                                            ABU97916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
                                                                         ABU97916
                                                           RESULT
                                                                                                  ò
                                               The present sequence is parvovirus non-structure protein 1 (NS1) variant (S283A). The invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoded by the double-stranded replicative form DNA of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide obtd. by recombinant DNA methods - for vaccination against parvovirus infections in man and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventors claim an immunologically active polypeptide for the development of vaccinal immunity against parvovirus infection. Also claimed are DNA sequences wholly or partly duplicative of defined sequences. The polypeptides are used in vaccines for conferring protection against parvovirus infections in man and animals. (Updated 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                ô
                                                                                                                                                                        96.1%; Score 99; DB 4; Length 672; 95.0%; Pred. No. 1.4e-07;
                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein envelope; immunogen; vaccine; antigen; epitope
transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Table II, Page 33-49; 80pp; English.
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine parvovirus; NADL-2 virulent strain.
                         Claim 6; Page 14-16; 41pp; English.
                                                                                                                                                                                                                                                                                                            AAP40306 standard; protein; 690 AA
                                                                                                                                                                                                                                        461 GQTIRIDQKGKGSKQIEPTP 480
                                                                                                                                                                                                                        1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84WO-US000063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83US-00459203
84US-00567968
                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                          2003 to correct OS field.)
                                                                                                                                                                                 Local Similarity 95.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1984-201354/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN40252
                                                                                                                                                 Sequence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO8402847-A
                                                                                                                                                                                                                                                                                                                                                          24-OCT-2003
12-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-1984
                                                                                                                                                                                                                                                                                                                                                                                                             parvovirus
                                                                                                                                                                                                                                                                                                                                   AAP40306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6;
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fox GM;
                                                                                                                                                                                                                                                                                              RESULT
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#X8X0000000X8
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Flaux M;

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The present invention relates to method for producing peptides, polypeptides, or proteins having a predetermined property. The method comprises (a) producing a population of sets of polymuclectide sequences that encode modified forms of a target protein, (b) introducing each set of polymucleotide sequences into host cells and expressing the encoded protein, where the host cells are present in an addressable array, and protein, where the host cells are present in an addressable array, and conseful in performing high throughput directed evolution of peptides and proteins, particularly those that act in complex biological settings, by rainants and for titering viruses. ABU97391-ABU97952 represent Adeno associated virus (AAV) mutant rep proteins used as an exemplification of the method of the invention. Note: The sequence data for this patent did electronic format directly from WIPO at the was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
Producing proteins with a predetermined property comprises introducing nucleic acids encoding a modified target protein into host cells and expressing and screening for proteins with different activity than the target protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.9%; Score 72; DB 6; Length 312; 65.0%; Pred. No. 0.0018; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                     Disclosure; SEQ ID NO 526; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GQAIRIDQKGKGSKQIEPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 312 AA;
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Gaps

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96.1%; Score 99; DB 1; Length 690; 95.0%; Pred. No. 1.4e-07; ive 0; Mismatches 1; Indels

19; Conservative

Query Match Best Local Similarity Matches 19; Conserv

ADB70945 standard; protein; 312 AA.

RESULT 9 4DB70945 (first entry)

04-DEC-2003

ADB70945;

us-10-069-056-17.rag

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The present invention relates to method for producing peptides,

CC omprises (a) proteins having a predetermined property. The method

CC comprises (a) producing a population of sets of polymucleotide sequences

CC that encode modified forms of a target protein, (b) introducing each set

CC of polymucleotide sequences into host cells and expressing the encoded

CC (c) individually screening the sets of encoded proteins. The method is

CC protein, where the host cells are present in an addressable array, and

CC protein, where the host cells are present in an addressable array, and

CC rational matagenesis. The method is also used for generating protein

CC rational matagenesis. The method is also used for generating protein

CC variants and for titering viruses. ABU97391-ABU97952 represent Adeno

associated virus (AAV) mutant rep proteins used as an exemplification of

CC the method of the invention. Note: The sequence data for this patent did

CC form part of the printed specification, but was obtained in

CC ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                              Producing proteins with a predetermined property comprises introducing nucleic acids encoding a modified target protein into host cells and expressing and screening for proteins with different activity than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutant; mutein; adeno-associated virus; AAV; anti-HIV; gene therapy; Rep 78; human papilloma virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.9%; Score 72; DB 6; Length 397; 65.0%; Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adeno-associated virus Rep mutant SEQ ID NO:524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 524; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB70943 standard; protein; 397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 GSAVRVDQKCKSSAQIDPTP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                              Flaux M;
                                                                                         .6-AUG-2002; 2002WO-IB003921
                                                                                                                                27-AUG-2001; 2001US-0315382P.
17-DEC-2001; 2001US-00022249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2001; 2001US-0315382P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                  (NAUT-) NAUTILUS BIOTECH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adeno-associated virus.
                                                                                                                                                                                                                                            Vega M, Drittanti L,
                                                                                                                                                                                                                                                                                          WPI; 2003-354538/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 397 AA;
WO2003023032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003018820-A2
                                                                                                                                                                                                                                                                                                                                                                                                        target protein.
                                           20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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  d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel adeno-associated virus (AAV), comprising an uncleic acid encoding the sequence comprising 19-621 amino acids, given in the specification. A virus of the invention has anti-HIV activity, and may have a use in gene therapy. The protein used in the invention is Rep Ps protein. The AAV is useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                     mutant; mutein; adeno-associated virus; AAV; anti-HIV; gene therapy; Rep 78; human papilloma virus; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide production; protein production; target protein; high throughput directed evolution; rational mutagenesis; AAV; protein variant generation; virus titering; Adeno associated virus; rep protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New adeno-associated virus, useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 7; Length 312; Pred. No. 0.0018; 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno associated virus (AAV) mutant rep protein #524
                                                                                                                                                                           Adeno-associated virus Rep mutant SEQ ID NO:526
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Claim 21; SEQ ID NO 526; 869pp; English

Drittanti L, Flaux M;

Vega M,

WPI; 2003-278671/27

(NAUT-) NAUTILUS BIOTECH

16-AUG-2002; 2002WO-IB004087. 27-AUG-2001; 2001US-0315382P. 17-DEC-2001; 2001US-00022390.

Adeno-associated virus.

Synthetic.

WO2003018820-A2.

06-MAR-2003

65.0%; Preq.

69.98;

Query Match Best Local Similarity 65.0 Matches 13; Conservative

Sequence 312 AA;

ð 셤 ABU97914 standard; protein; 397 AA

(first entry)

30-JUL-2003

ABU97914;

Adeno associated virus. Synthetic.

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Gaps

comprising

Gaps

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Length 397; 4; Indels

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a nucleic acid encoding the sequence comprising 19-621 amino acids, given in the specification. A virus of the invention has anti-HIV activity, and may have a use in gene therapy. The protein used in the invention is Rep 78 protein. The ApV is useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New library of fusion nucleic acids each encoding a Rep protein recognized by a nucleic acid modification enzyme and a candidate protein, useful for detecting protein-protein interactions, protein drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion nucleic acid library; Rep protein; tumour cell; apoptosis; nucleic acid modification enzyme; cell death; decreased cell growth; protein-protein interaction detection; cell division; cancer therapy;
                                                                                                             New adeno-associated virus, useful for preparing a composition for treating or inhibiting human papilloma virus or HIV infection.
                                                                                                                                                                                 a novel adeno-associated virus (AAV),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein drug discovery; pharmacogenetics; NS1 protein
                                                                                                                                                                                                                                                                                                                        Score 72; DB 7;
Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE,
                                                                                                                                                      Claim 21; SEQ ID NO 524; 869pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY97725 standard; protein; 461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 31; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 1 GQAIRIDQKGKGSKQIEPTP 20
                                                      Drittanti L, 'Flaux M;
                                                                                                                                                                                                                                                                                                                           69.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0150004P.
2000US-0209130P.
17-DEC-2001; 2001US-00022390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-2000; 2000WO-US022906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                  The invention relates to
                                                                                                                                                                                                                                                                                                                                                      13, Conservative
                           (NAUT-) NAUTILUS BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NS1 protein sequence.
                                                                                WPI; 2003-278671/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-218443/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or pharmacogenetics
                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goose parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA91315
                                                                                                                                                                                                                                                                                                  Sequence 397 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY97725;
                                                                                                                                                                                                                                                                                                                         Query Match
                                                      Vega M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li M;
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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This sequence is the goose parvovirus NS1 protein. The invention relates

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to a library of fusion nucleic acids, each encourny a new process. Candidate protein, a presentation structure, a targeting sequence or a label. The Rep protein is a nucleic acid modification enzyme. The random or directed libraries (including the cDNA libraries) can be introduced into any tumnour cell, and peptides identified which by themselves induce compositions may also be used to detect protein-protein interactions, protein drug discovery, particularly for protein drugs that interactions, protein drug discovery, particularly for protein drugs that interactions, protein drug discovery, particularly for protein drugs that conterned with targets on cell surfaces, to discover DNA or nucleic acid modification enzymes with decreased toxicity for the host cells, to dentify or generate Rep proteins with decreased toxicity, improved contents attachment sequences for use in expression vectors and in content cander therapy and in the content cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander cander can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS; enzyme attachment sequence; cancer therapy; protein-protein interaction; drug discovery; NS1 protein; gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library of nucleic acid/protein conjugates, has a fusion of nucleic acid modification enzyme and candidate compound, and expression vector having a fusion of nucleic acids encoding NAM enzyme and the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to genetic libraries of nucleic acid/
protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                             killing tumour cells. The methods can be combined with other cancer therapeutics (drugs or radiation) to sensitize cells and thus induce rapid and specific apoptosis, cell death, loss of cell division or decreased cell growth after exposure to a secondary agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.9%; Score 72; DB 4; 70.0%; Pred. No. 0.0028; iive 2; Mismatches 4
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nes 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (XENC-) XENCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goose parvovirus.
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Matches
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cector (with a fusion of nucleic acids encoding the enzyme and candidate vector (with a fusion of nucleic acids encoding the enzyme and candidate protein respectively), an enzyme attachment sequence (BAS; RNA sequence), where the candidate compound and candidate protein are different and BAS and the enzyme are covalently linked. The NAP conjugates are useful in screens to assay binding to target molecules and/or to screen candidate agents for the ability to modulate the activity of the target molecule. They are useful in cancer therapy. Sequences of the invention are also useful to detect protein-protein interaction, in drug discovery, to discover DNA or nucleic acid binding proteins, using nucleic acids as the targets and to screen for NAM enzymes with decreased toxicity for host care also useful in pharmacogenomic studies, for screening bioactive agents on surface cells, viruses and microbial organisms. They are also useful for screening proteins causing phenotypic changes such as alter attachment, infectivity, etc. of the virus. Sequences of the invention are also used in gene therapy. The present sequence is Goose parvovirus NSI protein used in the invention

Sequence 461 AA;

69.9%; Score 72; DB 5; Length 461; 70.0%; Pred. No. 0.0028; ive 2; Mismatches 4; Indels 232 GSAVRVDOKCKGSVCIEPTP 251 1 GOAIRIDOKGKGSKOIEPTP 20 Local Similarity 70.0 les 14; Conservative Query Match Matches 셤 ઠે

RESULT 14

AAE28649 standard; protein; 461 AA

AAE28649;

(first entry) 27-DEC-2002

Goose parvovirus NS1 protein.

Nucleic acid modification enzyme; NAM; enzyme attachment sequence; BAS; protein design automation; PDA; cancer; protein-protein interaction; infection; gene therapy; NSI protein.

parvovirus Goose

WO200268453-A2.

06-SEP-2002.

19-FEB-2002; 2002WO-US004853.

22-FEB-2001; 2001US-00792629.

(XENC-) XENCOR INC.

Li M, Dahiyat BI;

WPI; 2002-691653/74. N-PSDB; AAD46143 Generating a library of fusion nucleic acids for treating cancer or infection, or detecting protein-protein interaction, comprises providing computationally-derived library of candidate protein sequences and expression vectors.

Disclosure; Page 199-201; 246pp; English.

The present invention relates to a novel method of generating a library of fusion nucleic acids. The method involves providing a computationally-derived library of candidate protein sequences and creating a library of expression vectors containing a fusion nucleic acid having a sequence

a candidate protein acid modification (NAM) enzyme and a sequence encoding a candidate protein sequence from the library and an enzyme attachment sequence [RAS) that is recognised by the NAM enzyme. The invention also relates to the use of a variety of computation methods including protein dusion nucleic acids that may be used in treating cancer or infections, in detecting protein-protein interactions, discovery of DNA or nucleic acids that may be used in treating cancer or infections, in detecting protein-protein interactions, discovery of DNA or nucleic acid binding proteins, protein drug discovery, screening for NAM enzymes with decreased toxicity to the host cells and NAM enzymes/EAS pairs with increased affinity or in pharmacogenetic studies. The invention is also used in gene therapy. The present sequence is Goose parvovirus NS1 protein. This sequence is used to illustrate the method of the invention 8899999999998888

Sequence 461 AA;

Gaps . 0 69.9%; Score 72; DB 5; Length 461; 70.0%; Pred. No. 0.0028; ive 2; Mismatches 4; Indels Best Local Similarity 70.0 Matches 14; Conservative Query Match

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232 GSAVRVDQKCKGSVCIEPTP 251 1 GOAIRIDOKGKGSKQIEPTP 20 ठ 셤

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Gaps ö AAE26945 standard; protein; 461 AA.

AAE26945;

13-DEC-2002 (first entry)

Goose parvovirus NS1 protein.

Prokaryotic library, candidate protein; nucleic acid modification; NAM; enzyme attachment sequence; BAS; clinical pharmacology; chemical sensor; enzymology; cosmetic research; toxic; environmental safety assessment; nutrient biology; NS1.

Goose parvovirus

WO200266653-A2.

29-AUG-2002

14-DEC-2001; 2001WO-US049058.

14-DEC-2000; 2000US-0256163P

(XENC-) XENCOR INC

Li M, Liu Y;

WPI; 2002-667068/71. N-PSDB; AAD44605.

New library of prokaryotic pET-24a expression vectors, host cells or nucleic acid/protein conjugates, useful for screening candidate proteins and their nucleic acids or modification enzymes for pharmacogenetic analysis

Disclosure, Fig 31; 127pp; English.

The invention relates to methods and compositions for the construction of prokaryotic libraries expressing candidate proteins and the use of these libraries to identify candidate proteins and the nucleic acids encoding them. The invention provides a library of prokaryotic pET-24a vectors comprising a fusion nucleic acid consisting of a nucleic acid encoding a nucleic acid modification (NAM) enzyme or a candidate protein, or a nucleic acid acid acid encyment operably linked to the NAM enzyme or the candidate protein, and an enzyme attachment sequence (EAS) recognised by the NAM enzyme. The library is used for identifying candidate proteins and nucleic acids encoding these proteins, in screening for NAM enzymes

with decreased toxicity for the host cells, or in identifying novel or improved EASs, which may be used for understanding cellular processes or any subsequent thrarapeutic or toxic activities. The nucleic acid/protein (NAP) conjugates are useful in diagnostic assays and in research including clinical pharmacology, functional genomics, pharmacogenomics, agricultural chemicals, environmental safety assessment, chemical sensor, nutrient biology, cosmetic research or enzymology. These may also be used in in vitro screening techniques and in assays with target molecules. The present sequence is Goose parvovirus NSI protein used in the invention 88888888888

Sequence 461 AA;

0; Gaps Query Match
69.9%; Score 72; DB 5; Length 461;
Best Local Similarity 70.0%; Pred. No. 0.0028;
Matches 14; Conservative 2; Mismatches 4; Indels

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Search completed: May 28, 2004, 12:57:05 Job time : 48.5 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein May 28, 2004, 12:52:43; Search time 10.5 Seconds Run on:

(without alignments)
183.222 Million cell updates/sec

US-10-069-056-17 Perfect score: Title:

103 1 GOAIRIDOKGKGSKOIEPTP 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	noncapsid protein	noncapsid protein		noncapsid protein		noncapsid protein					noncapsid protein	noncapsid protein	probable pili chap	hypothetical prote	hisA protein - Cor	probable type II D	noncapsid protein	hypothetical prote	acriflavin resista	transcription regu	probable transcrip	insertion element	insertion element	probable insertion	probable transposa	hypothetical prote	ATP-binding transp	pectin methylester	amino acid transpo
SUMMARIES	ΙD	UYPV1F	UYPVPP	UYPVNA	A44276	UYPVCP	UYPVME	UYPVFP	UYPVV1	UYPV1M	UYPVIM	852209	UYADIA	AC0358	S77377	JE0213	G72659	UYPV19	T00382	AD3557	AI2997	H98285	H81802	F81855	E81858	H81889	AE3118	B98169	T04359	838111
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de	Query Match	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	6.69	65.0	46.6	44.7	44.7	44.7	44.7	44.2	٠	٠	43.2	٠	42.7	42.7	42.7	42.7	42.7	42.7	42.7
	Score	66	66	66	66	66	66	66	66	66	66	72	63	48	46	46	46	46	45.5	45	44.5	44.5	44	44	44	44	44	44	44	44
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penicillin-binding	noncapsid protein	cold-inducible RNA	hypothetical prote	amidophosphoribosy	protein ZK1127.7 [hemolysin (importe	IS1106 transposase	hypothetical prote	site-specific DNA-	NADH2 dehydrogenas	DNA topoisomerase	multidrug resistan	fibronectin - chic	vitellogenin precu	probable pectinest
S49570	UYPVAD	JC6571	S09825	A70401	C88196	AI0452	G81072	AB2112	S07792	A45456	AH2134	JC5667	A29355	JC4956	C84603
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	44	43	43	43	43	42.5	42	42	42	42	42	42	42	42	41.5
44															

ALIGNMENTS

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ESULT	R LVGV

noncapsid protein NS1 - feline panleukopenia virus (fragment) C;Species: feline panleukopenia virus, FPLV C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999

C;Accession: A03697
R;Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J. Virol. 55, 574-587, 1985
A;Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parv A;Reference number: A03697; MUID:85265017; PMID:2991581

A; Molecule type: DNA

A; Residues: 1-392 < CAR>

A,Cross-references: EMBL:M10824, NID:g333474; PIDN:AAA47160.1; PID:g333475 C;Superfamily: parvovirus noncapsid protein C;Keywords: noncapsid protein

Gaps ö Length 392; 1; Indels DB 1; 3e-08; Score 99; DB 1; Pred. No. 3e-08 Query Match 96.1%; Best Local Similarity 95.0%; Matches 19; Conservative (

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1 GOAIRIDOKGKGSKOIEPTP 20 ð d

186 GÓTIRIDQKGKGSKQIEPTP 205

noncapsid protein NS1 - porcine parvovirus (strain NADL-2)
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Species: porcine parvovirus: piaz-Aroca, E.; Casal, J.I.
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971

A; Molecule type: DNA A; Accession: A33302

A; Residues: 1-660 <RAN>

A; Crossing State of the control of

A; Molecule type: DNA A; Residues: 1.85, 7R, 87-273, 7R, 275-375, VV, 377-620, NLH', 623-624, PTPPD', 630, AIR', 634, A; Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989 C; Superfamily: parvovirus noncapsid protein C; Keywords: noncapsid protein

Query Match

96.1%; Score 99; DB 1; Length 660;

us-10-069-056-17.rpr

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R;Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.; Shinage J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone of the A;Reference number: A38350; WUID:91202123; PMID:2016597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Virol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine parvov
A;Reference number: A36608; WUID:91073139; PMID:2174965
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C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   noncapsid protein NS1 - mink enteritis virus (strain Abashiri)
C,Species: mink enteritis virus, MEV
C,Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
                                           noncapsid protein NS1 - canine parvovirus (strain N)
C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A29662
                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:M19296; NID:g333438; PIDN:AAA67459.1; PID:g333439
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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A;Residues: 1-668 <KAR>
A;Cross-references: 2-608 <KAR>
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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A;Residues: 1-668 <MAR>
A;Cross-references: GBXS5115; NID:g60863; PIDN:CAA38910.1; PID:g60864
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Pred. No. 5.2e-08;
0; Mismatches 1; Indels
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                                                                                                                                                     RiRed, A.P.; Jones, E.V.; Miller, T.J.
J. Virol. 62, 266-276, 1988
A;Titler: Nuclectide sequence and genome organization of A;Reference number: A29962; MUID:88062992; PMID:2824850
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 99; DB 1; 1
Pred. No. 5.2e-08;
0; Mismatches 1;
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Pred. No. 5.2e-08;
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Best Local Similarity 95.0%;
Matches 19; Conservative 0
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95.0%;
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ilarity 95.0%;
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les 19; Conserv
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Matches 19; Conserv
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A; Residues: 1-668 < REE>
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N'Alternate names: nonstructural protein NS-1
N'Alternate names: nonstructural protein NS-1
N'Alternate names: nonstructural protein NS-1
N'Alternate names: nonstructural protein NS-1
C;Beciss: parcine parvovirus
C;Beciss: parcine parvovirus
C;Beccession: A36217; A46472; A33743
C;Accession: A36217; A46472; A33743
N'Asudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 178, 611-616, 1990
A;Title: The complete nucleotide sequence of an infectious clone of porcine parvovirus, A;Reference number: A36217; MUID:91021005; PMID:2219713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bergeron, J.; Menezes, J.; Tijssen, P.
ViroLogy 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and translation products of
A;Reference number: A48472; MUID:94025614; PMID:8212598
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C;Species: parvovirus LullI
C;Species: parvovirus LullI
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 26-Feb-1999
C;Accession: A44276
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
A;Title: The complete nucleotide sequence of parvovirus LullI and localizati
A;Reference number: A44276; MUID:93297126; PMID:8517025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Wolecule type: DNA
X;Residues: 1-662 vYAS-
A;Cross-references: EMBL:M38367; NID:g332987; PIDN:AAA46920.1; PID:g332989
A;Experimental source: strain NADL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-662 <BER>
A;Experimental source: strain NADL-2, ATCC VR-742
A;Experimental source: strain NADL-2, ATCC VR-742
C;Superfamily: parvovirus noncapsid protein
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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                           Indels
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Pred. No. 5.2e-08;
0; Mismatches 1;
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Local Similarity 95.0%; Pred. No. 5.2e-08;
hes 19; Conservative 0; Mismatches 1;
     Pred. No. 5.1e-08;
                           0; Mismatches
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A;Residues: 1-668 - ODIP-
A;Cross-references: GB:M81888
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.; Tijssen, P.
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95.0%;
Best Local Similarity 95.0%;
Matches 19; Conservative
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A; Status: translation not shown
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J. Virol. 57, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986

J. Virol. S7, 656-669, 1986
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NiAlternate names: nonstructural protein NS1; NS1 protein
C.Species: muscovy duck parvovirus
C.Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
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N;Contains: noncapsid protein NS2
C;Species: adeno-associated virus type 2
C;Species: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jul-1999
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A;Cross-references: EMBL:X75093; NID:g609091; PIDN:CAA52983.1; PID:g609092
A;Experimental source: strain FM
                                                                                                                                                A;Residues: 1-645,'I',647-721 <AST>
A;Residues: 1-645,'I',647-721 <AST>
CXCross-references: EMBL:M12032; NID:g332289; PIDN:AAA69566.1; PID:g825477
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Zadori, Z.; Erdei, J.; Nagy, J.; Kisari, J.
submitted to the EMBL Data Library, September 1993
A;Reference number: $52209
A;Accession: $52209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: NS1
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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nes 12; Conserv
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A; Residues: 1-536 <SRI>
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Matches
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                                                                                                                                                                                                    noncapaid protein NS1 - parvovirus H1
C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: A03695
R;Rhode III, S.L.; Paradiso, P.R.
J. virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybri A;Reference number: A03695; MUID:83112183; PMID:6821009
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Cispecies: minute virus of mice, murine parvovirus
Cispecies: minute virus of mice, murine parvovirus
Cispecies: minute virus of mice, murine parvovirus
Cispecies A23008; A29510
Risahli, R.; McMaster, G.K.; Hirt, B.
Risahli, R.; Acids Res. 13, 3517-3531, 1985
A;Title: DNA sequence comparison between two tissue-specific variants of the autonomous A;Reference number: A23008; MUID:85242059; PMID:3855242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-672 <RHO>
A;Cross-references: EMBL:X01457; NID:g60993; PIDN:CAA25689.1; PID:g60994; EMBL:J02198
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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C; Species: minute virus of mice, murine parvovirus
C; Species: minute virus of mice, murine parvovirus
C; Accession: A03698
R; Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C.
Nucleic Acids Res. 11, 999-1018, 1983
A; Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus. A; Reference number: A03696; MUID:83143341; PMID:6298737
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-672 < AST>
A; Crose-references: EMBL:V01115
C; Superfamily: parvovirus noncapsid protein
C; Keywords: noncapsid protein
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R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.
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                                 GOTIRIDOKGKGSKOIEPTP 481
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A; Residues: 1-721 <SAH>
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A; Molecule type: DNA
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AC0358
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
11, M.; Rutherford, A.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R, Koneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystie
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: stationary-phase survival protein SurE
                                                                                                                                                                                                    probable pili chaperone protein YPO2944 [imported] - Yersinia pestis (strain CO92)
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A;Cross-references: GB:AL590842; PIDN:CAC92190.1; PID:g15980902; GSPDB:GN00175
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hisA protein - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: -1-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C;Accession: JE0213
R;Jung, S.I.; Han, M.S.; Kwon, J.; Cheon, C.I.; Min, K.H.; Lee, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein sll1459 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr_1997 #sequence_revision 25-Apr-1997 #text_change 02-Nov-2001
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A;Accession: S77377
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 4.1;
3; Mismatches
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C;Superfamily: chaperone protein papD
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47 QAIAVEQRGKNRYAVDGTP 65
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Best Local Similarity 57.1%;
Matches 8; Conservative
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169 NOKGRGVKVVNPTP 182
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A;Molecule type: DNA
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Biochem. Biophys. Res. Commun. 247, 741-745, 1998
A;Title: Cloning of the histidine biosynthetic genes of Corynebacterium glutamicum: Orgar A;Reference number: JE0213; MUID:98321198; PMID:9647764
A;Residues: 12013
A;Molecule type: DNA
A;Residues: 1-245 «JUN»
A;Residues: 1-245 «JUN»
A;Coss-references: GB:AF051846; NID:g2952537; PIDN:AAC05575.1; PID:g2952538
C;Genetics:
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sulfolobus
caenorhabdi
                                                          homo sapien
                         homo sapien
                                        oncorhynchu
                                                                             escherichia
   gallus gall
                                                                                                                                                                                                            pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=8255017; PubMed=2991581;
Carlson J., Rushlow K., Maxwell I., Maxwell F., Winston S., Hahn W.;
Carlson J., Rushlow K., Maxwell I., Maxwell F., Winston S., Hahn W.;
"Cloning and sequence of DNA encoding structural proteins of the autonomous parvovirus feline panleukopenia virus.";
J. Virol. 55:574-587(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBL_TaxID=10786;
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P11722
015440
092093
092093
0987026
P1976
P20665
P19257
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P19257
                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M10824; AAA47160.1; -.
PIR; A03697; UYPV1F.
InterPro; IPR001593; AAA ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.1%; Score 99; DB 1; Length 392; Best Local Similarity 95.0%; Pred. No. 4.1e-09; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
; B875ADDB4977F616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 AA.
                                                                                                                                                                                                                                                                                                                                                              392 AA
                                                                                                                                                                                                                                                                 ALIGNMENTS
 FINC_CHICK
MRPS_HUMAN
VIT_ONCMY
CHDS_HUMAN
PEMK_ECOLI
TRA6_NEIMB
PIV_MORBO
                                                                                                                                                MTSZ SHISO
TP6A SULSH
TOP2 CAEEL
R15E PYRAB
                                                                                                                                PIV MORLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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1437
1659
2713
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322
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379
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1520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology '183:195-205(1991).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                              J. Virol. 70:2508-2515(1996).
--- FUNCTION: Seems necessary for viral DNA replication.
--- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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"Nucleotide sequence of feline panleukopenia virus: comparison with canine parvovirus identifies host-specific differences.";
J. Gen. Virol. 71:2747-2753 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mapping specific functions in the capsid structure of canine
parvovirus and feline panleukopenia virus using infectious plasmid
                                                                                                                              Bergeron J., Hebert B., Tijssen P.; "Genome organization of the Kresse strain of porcine parvovirus: identification of the allotropic determinant and comparison with those of NADL-2 and field isolates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feline panleukopenia virus (strain 193) (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                          ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF01057; Parvo_NS1; \overline{1}. Nonstructural protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.1%; Score 99; DB 1; Length 662; 95.0%; Pred. No. 7.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
10-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75591 MW; B53F76D9F9FBD613 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
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    (strain Kresse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                        SEQUENCE FROM N.A.
MEDLINE=96183900; PubMed=8642680;
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STRAIN=193/70;
MEDLINE=91073139; Pubmed=2174965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001257; Parvo NS1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405
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      Porcine parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662 AA;
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                                          NCBI_TaxID=73487;
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Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.,
"The complete nucleotide sequence of an infectious clone of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).

G -> R (IN REF. 2).

K -> R (IN REF. 2).

C -> V (IN REF. 2).

TALTQHARFSNIDT -> NLHLTPTPPDSAIRTP (IN
                                                                                                                            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10797;
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Ranz A.I., Manclus J.O., Diaz-Aroca E., Casal J.I.;
"Porcine parvovirus: DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 367-660 FROM N.A. MEDLINE-90085785; PubMed-2596019; Assudevacharya J., Basak S., Srinivas R.V., Compans R.W.; "Nucleotide sequence analysis of the capsid genes and the riterminal palindrome of porcine parvovirus, strain NADL-2."; Virology 173:368-377(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 1; Length 660;
Pred. No. 7.2e-09;
0; Mismatches 1; Indels
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COBIDF2226A2EFOA CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
01-NOV-1990 (Rel. 16, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NSI).
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                                                                                                          Porcine parvovirus (strain NADL-2) (PPV)
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95.0%;
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AAA46916.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 parvovirus, strain NADL-2.
Virology 178:611-616(1990)
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Best Local Similarity 95.0°
Matches 19, Conservative
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86
274
376
634
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AC P52502;
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Query Match
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P36311;
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        between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Kariatsumari T., Horiuchi M., Hama E., Yaguchi K., Ishigurio N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
1-AUG-1992 (Rel. 23, Last sequence update)
15-DBC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
                                                                                                                                                                                                                                                         Score 99; DB 1; Length 668; Pred. No. 7.3e-09;
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                                                                                                                                                                    Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                1; Indels
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76736 MW; DBD5F9E92113685C CRC64;
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N -> D (IN REF. 2).

I -> V (IN REF. 2).

I -> N (IN REF. 2).
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Mink enteritis virus (strain Abashiri) (MEV)
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                            462 GÓTIRIDÓKGKGSKÓIEPTP 481
                                                                                                 EMBL, M38246; AAC37927.1; -.
PIR, A36608; UYPVFP.
INTERPRO; IPR003593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam, PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                                                      1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001257; Parvo NS1.
PEBAI, PF01057; Parvo_NS1, I.
SMART; SM00382; AAA, 1.
                                                                                                                                                                                                                                                          96.1%;
95.0%;
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                                                                                        EMBL; X55115; CAA38910.1; -.
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443
575
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P27438;
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SEQUENCE
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88062992; PubMed-2824850;
Reed A.P., Jones E.V., Miller T.J.;
"Nucleotide sequence and genome organization of canine parvovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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  Length 668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parrish C.R.;
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                           01-OCT-1989 (Rel. 12, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
15-DBC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
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01-JUN-1994 (Rel. 29, Last Sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1)
96.1%; Score 99; DB 1; I
95.0%; Pred. No. 7.3e-09;
ive 0; Mismatches 1;
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EMBL; M38245; AAB02798.1; -.
PIR; A29962; UYPVCP.
InterPro; IPR003593; AAA_ATPASE.
InterPro; IPR001257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
SMART; SM00392; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine parvovirus (strain N) (CPV)
                                                                                                                                              462 GQTIRIDQKGKGSKQIBPTP 481
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                                                                                                            1 GQAIRIDQKGKGSKQIEPTP 20
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                                                        Conservative
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nes 19; Conservative
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us-10-069-056-17.rsp

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ATP-binding.
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P03134;
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CONFLICT
SEQUENCE
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VNCS_MUMIV
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MEDLINE=85242059; PubMed=3855242;
Sahli R., McMaster G.K., Hirt B.;
"DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family
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MEDILINES 46115415; PubMed=3502703;

ARCELL C.R., Gardiner E.M., Tattersall P.;

"DNA sequence of the lymphotropic variant of minute virus of mice,

"DNA sequence of the lymphotropic variant of minute virus of mice,

"DNA sequence of the lymphotropic variant of protocype strain.";

T. Virol. 57:65-669(1986).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=35339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine minute virus (strain MVMi) (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                      MEDIINE=91297126; PubMed=8517025; Diffoot N., Chen K.C., Bates R.C., Lederma M.; The complete nucleotide sequence of parvovirus LuIII and localization of a unique sequence possibly responsible for its
                                                                                                                                                                                                                                                                                                                                                                                                                                             96.1%; Score 99; DB 1; Length 668; 95.0%; Pred. No. 7.3e-09; ive 0; Mismatches 1; Indels
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P07300; P10837;
01-APR-1988 (Rel. 07, Created)
01-JUL-1998 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                           Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autonomous parvovirus, minute virus of mice.";
Nucleic Acids Res. 13:3617-3633(1985).
-!- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                             -!- FUNCTION: Seems necessary for viral DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                     TP (POTENTIAL).
CAE69049F8F86B53 CRC64;
                                                                                                                                                                                                                                                                                                                 EMBL; M81888; -; NOT_ANNOTATED_CDS.
PIR; A44276; A44276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 GOTIRIDOKGKGSKOIEPTP 480
                                                                                                                                                                                                                                                                                                                                                                                                       ATP
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                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                  668 AA; 75846 MW;
                                                                                                                                  encapsidation pattern.";
Virology 192:339-345(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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EMBL; M12032; AAA69567.1; -.

InterPro; IPR001257. Barvo_NS1.

Pfam; PF01057; Parvo_NS1; I.

Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1996 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1)
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Nonstructural protein, Noncapsid protein, DNA replication,
ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                      Length 672;
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76248 MW; 50298F27662E3CID CRC64;
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672 AA; 76140 MW; 25F025FB328B4DF0 CRC64;
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Pred. No. 7.3e-09;
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95.0%; Pred. No. /...
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EMBL; V01115; CAA24309.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 GOTIRIDOKGKGSKOIEPTP 480
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MEDLINE=83143341; PubMed=6298737;
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Best Local Similarity
Local Similarity
Local 19; Conservative
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Best Local Similarity 95.0°
Matches 19; Conservative
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SEQUENCE
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P73440;
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YES9_SYNY3
STABBACCCC
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                                                                                                                                                                                                                               J. Virol. 45:173-184(1983).
-!- FUNCTION: Seems necessary for viral DNA replication.
-!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adeno-associated virus 2 (AAV2).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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                                                                                                                            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
                                                                                                                                                                                                       "Parvovirus genome: nucleotide sequence of H-1 and mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 56.1%; Score 99; DB 1; Length 672; Local Similarity 95.0%; Pred. No. 7.3e-09; les 19; Conservative 0; Mismatches 1; Indels
                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
Nonstructural protein; Noncapsid protein; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 ATP (PUIENLLAL).
75993 MW; 12F331142F72AAGD CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA replication protein (Noncapsid protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Virol. 45:555-564(1983).
-!- FUNCTION: ESSENTIAL FOR DNA REPLICATION.
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                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   genes by hybrid-arrested translation.";
J. Virol. 45:173-184(1983).
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-83112183; PubMed-6823009;
Rhode S.L. III, Paradiso P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 GOTIRIDOKGKGSKOIEPTP 480
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                         STANDARD;
                                                                                                               Hamster parvovirus H1.
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                                                                                                                                   NCBI_TaxID=10799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNCA AAV2
ID VNCA AAV2
AC P03132;
                         VNCS PAVHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIND
             PAVHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97061201; PubWed=8905231; Kaneko T., Asamizu E., Nakamura Y., Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto E., Nakamura Y., Kani M., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabatas S., Shimpo S., Takeuchi C., Sani S., Shimpo S., Takeuchi C., Sani T., Watanabe A., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)0 = an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alcohol + phosphate.
-!- COFACTOR: Magnesium (By similarity).
-!- SIMILARITY: Belongs to the surB acid phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 1; Length 536;
Pred. No. 0.0016;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                            334 341 ATP (POTENTIAL).
536 AA; 60754 MW; 7C1ECDD4E07703C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42CF7E02A02AECC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Hydrolase; Magnesium; Complete F METAL 8 MAGNESIUM (BY SIMILARITY) METAL 9 9 MAGNESIUM (BY SIMILARITY) METAL 37 37 MAGNESIUM (BY SIMILARITY) METAL 88 88 MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-ROV-1997 (Rel. 34, Last annotation update)
Putative acid phosphatase sll1459 (EC 3.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 GSKVRVDQKCKSSAQIDPTP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GOAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                              InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 MA
9 MA
37 MA
88 MA
120 PO
24907 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR., 577377; S77377.
HAMAP, MF 00060; atypical; 1.
InterPro; IPR002828; SurE.
                                                                                                                                                                                                                                                                               DNA replication; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                       65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD005378; SurE; 1.
TIGRFAMS; TIGR00087; surE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90906; BAA17480.1; -.
                                                                                                                                                 EMBL; J01901; AAA42372.1; -.
PIR; A03694; UYADIA.
                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 60.09
Marches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01975; SurE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
120 1
225 AA;
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CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 13:1572-1579 (2003).
-!- CATALVITC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino] imidazole-4-carboxamide = !
[(5-phosphoribosylamino) methylideneamino] -1-(5-phosphoribosyl) imidazole-4-carboxamide.
-!- PATHWAY: Histidine biosyrthesis; fourth step.
-!- SATHWAY: Histidine biosyrthesis; fourth step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the hisA / hisF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1-OCT-2003 (Rel. 45, Last annotation update)
1-(5-phosphoribosyl) -5-[(5-phosphoribosylamino)methylideneamino]
imidazole-4-carboxamide isomerase (EC 5.3.1.16)
                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.7%; Score 46; DB 1; Length 246; 45.0%; Pred. No. 2.7;
                          DB 1; Length 225;
                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Arverse Handap, Mr 201014; -; 1.

Handap, Mr 201014; -; 1.

InterPro; IPR006063; His4.

InterPro; IPR006062; His biosynth.

Pfam; PF00977; His biosynth; 1.

TIGREPHS; TIGRER0007; TIGRER0007; 1.

Isomerase; Histidine biosynthesis; Complete proteome.

246 AA; 26624 MW; EF62454178C09B50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
       44.7%; Scor.
42.1%; Pred. No. 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GOAVRLDOGEAGTEKSYGTP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                |||| ::|:||
QAIAVEQRGKNRYAVDGTP 65
                                                                                                                   2 QAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP005220; BAC18806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.0%;
Query Match
Best Local Similarity 42.1.
Best Local Similarity 62.1.
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                                                                                                                                                                                                                                                                                       STANDARD;
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tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HISA OR CE1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       efficiens.";
                                                                                                                                                                                                                                                       HIS4_COREF

ID HIS4_COREF

OG 08FWZ7,

DT 10-OCT-2003

DT 10-OCT-2003

DE 10-OCT-2003

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Matches
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ dateabases.
-!- CATALYTIC ACTIVITY: 1 - (5-phosphoribosyl) -5-[(5-phosphoribosyl) -5-[(5-phosphoribosylamino) methylideneamino] imidazole-4-carboxamide = 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)
imidazole-4-carboxamide isomerase (EC 5.3.1.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                             (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
                                                                                                                                                                                                                                                                    Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G -> S (IN REF. 1).

ERA -> DTQ (IN REF. 1).

A -> L (IN REF. 1).

RYGEKLAND -> AMARELLS (IN REF. 1).

R -> C (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.7%; Score 46; DB 1; Length 246; 45.0%; Pred. No. 2.7; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 13059 / AS019;
Jung S.I., Han M.S., Park Y.J., Lee M.-S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6A35CF9153C32B1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF 01014; -; 1.
InterPro; IPR003009; FMN_enzyme.
InterPro; IPR006063; His4.
InterPro; IPR006062; His4.
InterPro; IPR0090662; His Prosynth.
Fram, PR00977; His biosynth; 1.
IIGRPAMs; TIGR00007; TIGR00007; 1.
ISOMerase; Histidine biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF.
246 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIVA -> TYLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF051846; AAC05575.1; -. EMBL; AP005280; BAB99489.1; -. PIR; JE0213; JE0213.
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                                                      (Rel. 41, Created)
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157
195
246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                HISA OR CGL2096.
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TP6A AERPE
ID TP6A AERPE
AC Q9YE67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-1- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
-1- SUBUNIT: Heterotetramer of two subunits A and two subunits B (By
                                                                                                                                                                                                                                                           Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Rubota G., Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [somerase; Topoisomerase; DNA-binding; Metal-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Relaxes both positive and negative superturns and exhibits a strong decatenase activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.7%; Score 46; DB 1; Length 385; 45.0%; Pred. No. 4.3; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 103 DNA CLEAVAGE (BY SIMILARITY)
204 204 MAGNESIUM (BY SIMILARITY).
256 256 MAGNESIUM (BY SIMILARITY).
385 AA; 45012 MW; 19CBCB88728F3D37 CRC64;
                                                                                                               Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Dosulfurococcaceae, Aeropyrum.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
TOPE II DNA topoisomerase VI subunit A (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the TOP6A family.
                                                                                                                                                                                                                                                                                                                                                                                                     crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                             MEDLINE=99310339; PubMed=10382966;
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HAMAP, MF_00132, -, 1.
InterPro, IPR004085, DNA_top6A.
InterPro, IPR002815; DNA_top11.
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PRINTS; PR01552; TPISMRASEGA.
ProDom; PD008669; DNA_topli;
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nes 9; Conservative
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=56636;
                                                                                                       Aeropyrum pernix
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1 GQAIRIDQKGKGSKQIEPTP 20

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pig-tailed simian parv rhesus maca

chipmunk pa adeno-assoc hamster par

adeno-assoc adeno-assoc avian adeno

adeno-assoc

Title: Perfect score:

on:

Run

Sequence:

Scoring table:

Searched:

Database

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STRAIN=Yale,
MEDLINE=Z1102993; PubMed=11172095;
MEDLINE=Z1102993; PubMed=11172095;
MEDLINE=Z11029991; PubMed=11172095;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
Divergent replication kinetics of two phenotypically different parvoviruses of rats.";
J. Gen. Virol. 82:537-540(001).
EMBL, AR317513; AAC7438.1; -.
Interpro; IPR001257; Parvo_NS1.
Interpro; IPR01057; Parvo_NS1.
SEQÜENCE 397 AA, 43959 MW; D62052E4767366BB CRC64;
                                                                                                                                                                                                                                                                                                                     Autonomous rat parvovirus RV-Y.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=155025;
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96.1%; Score 99; DB 12; Length 397;
Best Local Similarity 95.0%; Pred. No. 5.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels
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Last annotation update)
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0667463
0667310
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Q67671
Q83288
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SEQUENCE FROM N.A.
071159
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feline pan]
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                                                         (without alignments)
197.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 feline
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Q83429 Q
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P89515
P90449
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                                                  May 28, 2004, 12:52:08 ; Search time 32 Seconds
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                 1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                 Post-processing: "Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    OM protein - protein search, using sw model
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O71159
P89516
P89515
P90449
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P906472
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Q8JV18
P88899
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Q8JV28
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1 GQAIRIDQKGKGSKQIEPTP
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sp_fungl:*
sp_fungl:*
sp_invertebrate:*
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sp_organelle:*
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sp_unclassified:*
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sp_bacteriap:*
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sp_virus:*
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Match 1
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Gaps

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Score

Result No.

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Horiuchi M.;
"Evolutionary pattern of feline panleukopenia virus differs from that
                    Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae, Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nonstructural protein 1.
Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 668;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                             of canine parvovirus.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, AB000057; BAA1901B.1;
GO; GO;000166; F:nucleotide binding; IEA.
InterPro; IPR0013593; AAA_ATPase.
InterPro; IPR001257; Parvo_NS1.
Pfam; PP01057; Parvo_NS1; I.
SNART; SM00382; AAA; I.
SEQUENCE 668 AA; 76741 MW; 2413E450EC9161BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horiuchi M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000069; BAA19030.1; -.
EMBL; AB0000605; BAA19024.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
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SMART; SM00382; AAA, 1.
Nonstructural protein.
Nonstructural AA; 76769 MW; OECAFEGBF62A5DEO CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99; DB 12;
Pred. No. 9.8e-08;
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Pfam; PF01057; Parvo NS1; 1.
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95.0%;
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Best Local Similarity 95.0°
Matches 19, Conservative
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hes 19; Conservative
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                                                                                     NCBI_TaxID=10786;
                                                                                                                                                     STRAIN=PLI-IV;
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                                                                                                                                                                                                                                                                                                          "Rat parvovirus type 1: the prototype for a new rodent parvovirus
                                                                                                                          Viruses, ssDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.
NCBI_TaxID=12441;
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Viruses; BSDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10786;
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Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
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Pred. No. 9.7e-08;
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR01257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; Ī.
SWART; SM00382; AAA; 1.
SEQUENCE 668 AA; 76755 MW; 37ABDFD347017F52 CRC64;
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                      Last sequence update)
Last annotation update)
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(TrEMBLrel. 25, Last annotation update)
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  01-AUG-1998 (TrEMBLrel. 07, Created)
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                                                               Nonstructural protein (Fragment)
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EMBL, AF036711, AA-40695.1; -.
InterPro, IPR001257; Parvo NS1.
Ffam, PF01057, Parvo NS1. 1.
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T virol. 72:3289-3299(1998).
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95.0%;
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ID P89515 PRELIMINARY;
AC P89515, DT 01-MAY-1997 (TrEMBLrel. 03, DT 01-MAY-1997 (TrEMBLrel. 03,
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                        01-AUG-1998 (TrEMBLrel. 07
01-DEC-2001 (TrEMBLrel. 19
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                                                                                                            Kilham rat virus
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01-OCT-2003
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Horiuchi M.;
"Evolutionary pattern of feline panleukopeina virus differs from that of canine parvovirus.";
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Horiuchi M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000060; BAA19021.1;
                                                                                                                                                                                     Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                          668 AA; 76770 MW; C8D6BDD0AE22183E CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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96.1%; Score 99; DB 12;
Best Local Similarity 95.0%; Pred. No. 9.8e-08;
Matches 19; Conservative 0; Mismatches 1
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EMBL; AB000049; BAA19010.1; -.
EMBL; AB000058; BAA19010.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR001257; Parvo NS1.
Ffam; PF01057; Parvo NS1.
SMART; SM00382; AAA; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Feline panleukopenia virus (FPV)
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Nonstructural protein.
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        NCBI_TaxID=10786;
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                                                                                STRAIN=A01;
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P90484;
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Feline panleukopenia virus (FPV).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=10786;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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NCBI_TaxID=10786;
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                                                                                                                                                                             Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000067; BAA19028.1; -.
EMBL; AB000065; BAA19026.1; -.
GO; GO:0019012; C:virion; IEA.
GO; GO:0010166; F:nucleotide binding; IEA.
InterPro; IPR001557; AAA ATPase.
InterPro; IPR00157; Parvo NS1.
Pfam; PF01057; Parvo NS1; I.
SMART; SM00382; AAA; I.
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, AB000015.
EMBL, AB000016.
EMBL, AB000016.
EMBL, AB000016.
InterPro; IPR001593; AAA ATPase.
InterPro; IPR001297; Parvo NSI.
Pfam; PF01057; Parvo NSI.
SMART; SM001382; AAA; 1.
SEQUENCE 668 AA; 76743 MW; 84A210104D9D5788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Nonstructural protein.
SEQUENCE 668 AA; 76755 MW; 008CED50178833EF CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Feline panleukopenia virus (FPV)
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                                                                                                                                     STRAIN=TU4;
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"Rat parvovirus type 1: the prototype for a new rodent parvovirus
                                  Rat parvovirus 1a.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=74581;
                                                                                                                        Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
                                                                                                                                                                                                                                                        Query Match 96.1%; Score 99; DB 12; Length 671; Best Local Similarity 95.0%; Pred. No. 9.8e-08; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                     EMBL, AF036710; AAC40693.1; -.
InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; 1.
SEQUENCE 671 AA; 75752 MW; 9BCB39A39298D4DE CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                             SEQUENCE FROM N.A. MEDLINE=98184569; PubMed=9525656;
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J. Virol. 72:3289-3299(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Nonstructural protein 1.
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               Nonstructural protein.
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                                                                                                                                   Horiuchi M., Goto H., Ishiguro N., Shinagawa M.; "Mapping of determinants of the host range for canine cells in the genome of canine parvovirus using canine parvovirus/mink enteritis virus chimeric viruses."; J. Gen. Virol. 75:1119-1128(1994).

EMBL; D26079; BAA05072.1;
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                                                  Horiuchi M.,
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
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GO; GO.0000166; F:nucleotide binding; IEA.
INTERPO; IPR003593; AAA AIPase.
INTERPO; IPR001257; Parvo_NS1.
FPfam; PF01057; Parvo_NS1; Ī.
SMART; SM00382; AAA; I.
SEQUENCE 668 AA; 76724 MW; C038269E428612B3 CRC64;
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InterPro; IPR001257; Parvo NS1.
Pfam, PF01057; Parvo NS1; 1.
SWART; SM00382; AAA; 1.
SEQUENCE 668 AA, 76755 MW; 1D72C5E85DBA430F CRC64;
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Feline panleukopenia virus
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Matches 19; Conservative
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NCBI_TaxID=10788;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI TaxID=12441;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=172385;
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MEDLINE-22120170; PubMed=12124471;
MED.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
Man (H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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95.0%; Pred. No. 9.8e-08;
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MEDLINE=9436551; PubMed=8083985;
Ball-Goodrich L.J., Johnson E.;
"Molecular characterization of a newly recognized mouse parvovirus.";
J. Virol. 68:6476-6486(1994).
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=35340;
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96.1%; Score 99; DB 12; Length 672;
Best Local Similarity 95.0%; Pred. No. 9.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                    Brown D.W., Like A.A.;
Brown D.W., Like A.A.;
"Sequence of a Diabetogenic Parvovirus of Rats.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
BMBL; UJ9033; AAB18326.1;
InterPro; IPROF157; Parvo NS1.
Pfam; PF01057; Parvo NS1.
SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
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SEQUENCE FROM N.A.
Ball-Goodrich N.A.
Submitted (UUL-1994); to the EMBL/GenBank/DDBJ databases.
EMBL; U12469; AAA61405.1; -
EMBL; U12469; AAA61405.1; -
EMBL; PPPO1057; Parvo NS1.
Pfam; PPPO1057; Parvo NS1.
SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                             GOAIRIDQKGKGSKQIEPTP 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                  Run on:
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5222, A 4323, Ap 4323, Ap 30326, A 30326, A 30326, A 30126, A 30109, A 30109, A 30109, A		24e = Gaps	
sednence sed		64685 ,	
		ce; No. gth 312 Indels	
223 23 23 88684 10326 10326 2014 20109	SOF	Sequen ; Len ; 5;	
7.25	ENTS S THEREOF	ficial ficial DB coo	SES THEREOF 594B
US-09-107-532A-5229 US-09-107-532A-5229 US-09-521-991A-28684 US-09-252-991A-308684 US-08-695-355-1 US-08-695-355-3 US-08-691-869-3 US-09-063-869-3 US-09-063-869-3 US-09-252-991A-28234 US-08-08-688A-2 US-08-08-688A-2 US-08-252-991A-2014 US-09-252-991A-2702 US-09-252-991A-2702 US-09-252-991A-2702 US-09-252-991A-2702 US-09-252-991A-2702 US-09-252-991A-22702	ALIGNMENT. 94B. AND USES T. 9/532,594B	n of Artificial construct votein 40 Score 67; DB Pred. No. 0.00 3; Mismatches	20 191 94B AND USES 9/532,594 rsion 4.0
		_ U O 0 44 *	EPTP
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10040 999 1777 1777 1777 1777 1777 1777 1777	ion Ufficat	ial Sequences in Description is synthetic sature in AAV4 Rep 65.0%;	KCKGSI U U
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9 18524 18720N 1870N 100rini,	T Artificial Sequence FORWATION: Descript: FORWATION: Synthetic FORWATION: AAV4 Rep 4B-8 Similarity 60.0% Similarity 60.0%	GGAIRIDOKGKGSKOIEPTP
6.444444444444444444444444444444444444	-594B-(e 8, Ag No 10 No 84B-(f 8) Ag No 84B-(f 8) Ag No 10 N	TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of As OTHER INFORMATION: Synthetic constru NAME/KEY: misc_feature OTHER INFORMATION: AAV4 Rep protein 9-532-594B-8 ery Match 65.0%; Score set_local Similarity 60.0%; Pred. tches 12; Conservative 3; Mis	1 0 (1) (1) (2) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4
/	RESULT 1 US-09-532-594B-8 Sequence 8, Application US/09532594B Patent No. 646854 APPLICANT: Chorini, John A. APPLICANT: Kotin, John A. APPLICANT: Rotin, About WECTOR AND USES TH TITLE OF INVENTION: AAV4 WECTOR AND USES TH TITLE OF INVENTION: AAV4 WECTOR AND USES TH TITLE OF INVENTION: AAV4 WECTOR AND USES TH CURRENT APPLICATION NUMBER: US/09/532,594B CURRENT FILING DATE: 2000-03-22 NUMBER OF SEQ ID NOS: 22 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3.9	S-O Mae	Qy 1 GQAIRIDQKGKGSKQIEPTP 20
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Sequence 19329, A Sequence 19264, A

Sequence 5, Sequence 5, Sequence 5,

Sequence 17, Appl Sequence 5503, Ap Sequence 4150, P Sequence 22466,

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RESULT 6
US-09-328-352-8111
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OTHER INFORMATION: synthetic construct
NAMMS/KEX: misc feature
CHER INFORMATION: AAV4 Rep protein 68
US-09-532-594B-10
                                                                                                   OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e; OTHER INFORMATION: synthetic construct
NAMMS/KEY: misc_feature
1 OTHER INFORMATION: AAV4 Rep protein 52
US-09-532-5948-9
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Pred. No. 0.0052;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09532594B
; Sequence 2, Application US/09532594B
; Patent No. 646824
; GENERAL INFORMATION:
; APPLICANT: Chorini, John A.
; APPLICANT: Kotin, Robert M.
; APPLICANT: Safer, Brian
; APPLICANT: Baider, Brian
; APPLICANT: Davidson, Beverly
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; TITLE OF INVENTION: AAV4 VECTOR AND USES
; CURRENT APPLICATION UNDMER: US/09/532,594B
; CURRENT APPLICATION UNDMER: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 623
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chorini, John A.
APPLICANT: Chorini, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                65.0%; Scor.
60.0%; Pred. No. v...
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                       172 GSKVRVDQKCKSSAQIDPTP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 GSKVRVDÓKCKSSAQIDPTP 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                           TYPE: PRT .
ORGANISM: Artificial Sequence
                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0%
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Best Local Similarity 60.0*
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SEQ ID NO 9
LENGTH: 399
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                                                                                 FEATURE:
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Sequence 8111, Application US/09328352

Sequence 8111, Application US/09328352

Sequence 811, Application US/09328352

Factor No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8111

LENGTH: 730
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NAME/KSY: misc feature
1 NAME/KSY: misc feature
1 OTHER INFORMATION: AAV4 Rep protein 78
US-09-532-594B-11
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OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e; OTHER INFORMATION: synthetic construct; NAME/KEY: misc_feature; NAME/KEY: misc_feature; OTHER INFORMATION: AAV4 Rep protein (full length)
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                                                                                                                                               Score 67; DB 4; Length 623;
Pred. No. 0.0085;
3; Mismatches 5; Indels
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Pred. No. 0.0085;
3; Mismatches 5; Indels
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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
IITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.7%; Score 45; DB 4;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 7; Conservative 5; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 11
LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-322-594B-11
Sequence 11, Application US/09532594B
Patent No. 6468524
                                                                                                                                                                                                                                                                                   396 GSKVRVDQKCKSSAQIDPTP 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                  Query Match
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.0%;
Best Local Similarity 60.0%;
Matches 12; Conservative
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Matches
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Patent NO. 6682597
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Gu, Wei
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-190001
CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT FILING DATE: 2002-06-04
                                                                                                                                                                       Gaps
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                                                                                                            40.8%; Score 42; DB 3; Length 1437;
46.2%; Pred. No. 2.5e+02;
ive 6; Mismatches 1; Indels
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PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/279, 281
PRIOR APPLICATION NUMBER: US 60/290, 289
PRIOR APPLICATION NUMBER: US 60/290, 289
PRIOR FILING DATE: 2002-03-28
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-13
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 1437
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PRIOR APPLICATION NUMBER: US 09/875,321
PRIOR PILING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR PELING DATE: 2000-06-05
PRIOR PELING DATE: 2001-06-05
PRIOR PELING DATE: 2001-06-05
PRIOR PELING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR PLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR PLING DATE: 2001-06-05
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PRIOR APPLICATION NUMBER: US 09/928,530
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/10162012
                                                                                                                                                                                                                                                          828 GQLVQLEEKGQGS 840
                                                                                                              Query Match
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                        1 GQAIRIDQKGKGS 13
                            , MOLECULE TYPE: protein US-09-061-400-2
TOPOLOGY: linear
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US-10-162-012-38
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Patent No. 651795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILLE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/094,190

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 476
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Sequence 2, Application US/09061400

Sequence 2, Application US/09061400

Sequence 2, Application US/09061400

Sequence 2, Application US/09061400

TITLE OF INVENTION: POLYPEPTIDE

NUMBER OF SEQUENCES: 8

CORRESPONDENCES: 8

CORRESPONDENCES: 8

CORRESPONDENCES: 8

CORRESPONDENCES: 8

CORRESPONDENCES: 8

COUNTRY: Boston

STATE: Assachusetts

COUNTRY: USA

ZIP: 0210

COUNTRY: USA

ZIP: 120

COUNTRY: USA

ZIP: 120

COUNTRY: BEADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPTER: BEADABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPTER: Ploppy disk

CONFATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION UNBER: USA

STATE: A-APRIL-1998

CLASSIFICATION NUMBER: USA

ATTORNEY/AGENT INFORMATION:

MAME: Blizabeth A. Hanley

REFERENCE/DOCKET NUMBER: MNI-056CP

TELECOMMUNICATION INFORMATION:

TELEBOHONE: (617) 227-7400

TELEBOHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 4; Length 476;
Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                 :|:||| :| ::||
608 LDKKGKKAKTVDPT 621
                                  6 IDQKGKGSKQIEPT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 DQRGRRSRGIQPDP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 DOKGKGSKQIEPTP 20
                                                                                                                                                                                              -09-252-991A-17887
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09347798
Patent No. 6242256
GENERAL INPORMATION:
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GOGTRLGYKGPKGSFEIEGT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.8%;
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1453 amino acids
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844 GQLVQLEEKGQGS 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GQAIRIDQKGKGS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-134-001C-4848
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; Sequence 2, Application US/08843459A
; Patent No. 6162616.
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
  DB 4; Length 1437;
                                                                                                                                                                                                                    Sequence 2, Application US/09001273
Patent No. 5994130
GENERAL INFORMATION:
APPLICANT: SHYAN, Andrew
TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teeta, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1453;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001, 273
                   2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5e+02;
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40.8%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.8%; Score 42; 46.2%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALFLACATION:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FERTON, G111an M
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIL-(
TELECOMMUNICATION INFORMATION:
TRIEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                     | | :::::||:|
828 GQLVQLEEKGQGS 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || :::::||:||
844 GQLVQLEEKGQGS 856
                                                                                1 GQAIRIDQKGKGS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GOAIRIDOKGKGS 13
                   Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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US-08-843-459A-2
                                                                                                                                                                                                       US-09-001-273-2
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  Query Match
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Sequence 4848, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4848
LENGTH: 404
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40.3%; Score 41.5; DB 4; Length 404;
Best Local Similarity 55.0%; Pred. No. 75;
Matches 11; Conservative 2; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1453;
CURRENT APPLICATION DATA:

SOFTWARE: PATENTING STATEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: U5/08/843,459A
FILING DATE: 16-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Hanley, Elizabeth A.

REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MAI-056 (formerly MIL-001)
TELECOMMUNICATION INFORMATION:

TELECHONE: (617)227-7400
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ. 1D NO:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 3; 1
Pred. No. 2.5e+02;
6; Mismatches 1;
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                                                                                                                      Query Match 39.8%; Score 41; DB 1; Length 363; Best Local Similarity 35.0%; Pred. No. 80; Matches 7; Conservative 4; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTR:

ZIP: 10532

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING PATE: 01-UJN-1995
FILING PATE: 01-UJN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
FUCR APPLICATION DATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elimer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                99 GÓCVHÍPGHNOAVRÓLEPVP 118
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                                                                                                                                                                                                                      1 GQAIRIDQKGKGSKQIEPTP 20
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08456837
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lam, Stephen Ting
Hammer, Phillip E.
Uknes, Scott Joseph
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TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 363 amino acids
amino acid
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; MOLECULE TYPE: protein
US-08-456-837-5
                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-258-2618-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO
       amino acid
XGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5643774
GENERAL INFORMATION:
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Pred. No. 79;
0; Mismatches 8; Indels
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APPLICATION NUMBER: US/08/258,261B FILING DATE: 08-UN-1994
CLASSIFICATION NUMBER: US 08/457,205
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
ATTORNEY/AGENT INFORMATION:
NAME: BLARE, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
FILE REFERENCE: BB-1174-B
CURRENT APPLICATION NUMBER: US/09/347,798
CURRENT PILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/093,209
HALLIER PILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Ciba-Geigy Corporation
: 7 Skyline Drive
Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08258261B
Patent No. 5639949
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 GVAİRİGGMAKĞSGMİHP 241
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TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 363 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: UNSURE
; LOCATION: (288)
US-09-347-798-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-258-261B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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99 GQCVHIPGHNQAVRQLEPVP 118

Search completed: May 28, 2004, 13:02:04 Job time: 13.5 secs

Appl Appl Appl Appl Appl

Sequence 29, Sequence 35 Sequence 29

Sequence 25, A Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 21, Sequence 31,

Sequence 33, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 13, Appli Sequence 13, Appli Sequence 9, Appli Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

Sequence 15, Sequence 9,

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB Maximum DB M

Database

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Sequence 526, Application US/1002390

Publication No. US20030129203A1

GENERAL INFORMATION:
APPLICANT: Vega, Manuel
APPLICANT: Plaux, Mariorie
TITLE OF INVENTION: MOTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES
FILE REFERENCE: 3781-912
CURRENT APPLICATION NUMBER: US/10/022,390
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR PILING DATE: 2001-8-27
NUMBER OF SEQ ID NOS: 735
SOFTHARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 526
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Mutant rep protein: rep40 153 398 AGC GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.9%; Score 72; DB 14; Length 312; 65.0%; Pred. No. 0.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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US-09-953-351-29
US-10-081-351-29
US-10-097-100-29
US-10-097-100-29
US-09-792-630-25
US-09-953-351-25
US-09-953-351-25
US-09-953-351-25
US-09-953-351-25
US-10-080-376-27
US-10-080-376-27
US-10-080-376-27
US-10-081-27
US-10-081-27
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US-10-081-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 526, Application US/10022249; Publication No. US20030134351A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:|:||| | ||:|||
172 GSAVRVDQKCKSSAQIDPTP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GOAIRIDOKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 65.0%
les 13; Conservative
   RESULT 2
US-10-022-249-526
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Sequence 525, App
Sequence 523, App
Sequence 523, App
Sequence 29, Appl
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Sequence 526, App
Sequence 524, App
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 525, Appl
Sequence 525, Appl
Sequence 525, Appl
Sequence 525, Appl
                                                                                                May 28, 2004, 12:57:09; Search time 34.75 Seconds (without alignments) 160.719 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-022-249-526

US-10-022-249-524

US-10-022-249-524

US-09-792-30-31

US-09-792-30-31

US-10-080-376-31

US-10-080-376-31

US-10-080-376-31

US-10-082-631

US-10-022-249-525

US-10-022-390-523

US-10-022-390-523

US-10-022-390-523

US-10-022-390-523

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                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                1151071 seqs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
                                                                                                                                                                                          1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Gaps

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Score

Result Š. 1224327

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NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 4.0
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                      SOFTWARE: Fast
SEQ ID NO 524
LENGTH: 397
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US-09-792-630-31
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              APPLICANT: Drittent, Lila
TITLE OF INVENTION: HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS
FILE REFERENCE: 37851-911
CURRENT APPLICATION NUMBER: US/10/022,249
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR PILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
SOFTWARE: RastSEQ for Windows Version 4.0
SEQ ID NO 526
LENGTH: 312
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APPLICANT: Vega, Manuel
APPLICANT: Dritanti, Lila
TITLE OF INVENTION: HOT THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS
FILE REPERENCE: 37851-911
CURRENT APPLICATION NUMBER: US/10/022,249
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR FILING DATE: 2001-08-27
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APPLICANT: Vega, Manuel
APPLICANT: Vega, Manuel
APPLICANT: Pritanti, Lila
APPLICANT: Plaux, Marjorie
TITLE OF INVENTION: MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES
FILE REFERENCE: 37851-912
CÜRRENT APPLICATION NUMBER: US/10/022,390
CÜRRENT FILING DATE: 2001-12-17
PRIOR PPLICATION DATE: 2001-12-17
PRIOR PILING DATE: 2001-08-27
                                                                                                                                                                                                                                                                                                                                           . OTHER INFORMATION: Mutant rep protein: rep40 153 398 AGC GCG US-10-022-249-526
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 69.9%; Score 72; DB 14; Length 312; Best Local Similarity 65.0%; Pred. No. 0.003; Matches 13; Conservative 3; Mismatches 4; Indels
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Best Local Similarity 65.0%; Pred. No. 0.00
Matches 13; Conservative 3; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 524
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 524, Application US/10022390 Publication No. US20030129203A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 524, Application US/10022249; Publication No. US20030134351A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GOAIRIDOKGKGSKOIEPTP 20
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                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-022-249-524
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Sequence 31, Application US/09953351
Publication No. US20030036643A1
GENERAL INFORMATION:
APPLICANT: Liu, Min
APPLICANT: Liu, Hong-Xiang
APPLICANT: Jiu, Hong-Xiang
APPLICANT: Jiu, Hong-Xiang
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APPLICANT: Jiu, Hon
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Patent No. US20020168640A1
GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Li, Min
CURRENT APPLICATION UNWERS: US/09/792,630
CURRENT APPLICATION NUMBER: US/09/792,630
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
LENGTH: 461
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                                                                                                                                 OTHER INFORMATION: Mutant rep protein: rep52 153 398 AGC GCG
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                                                                                                                                                                                                                                                                                                                                                                4; Indels
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Pred. No. 0.0039;
3; Mismatches 4
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Pred. No. 0.0046;
2; Mismatches 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 GSAVRVDQKCKSSAQIDPTP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 GSAVRVDQKCKGSVCIEPTP 251
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative
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Conservative
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US-09-792-630-31
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US-09-953-351-31
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Best Local Similarity
Matches 14; Conserv
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APPLICANT: Melander, Christian
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Hong-Xiang
APPLICANT: Liu, Cheng He
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FUSION LJ
FILE REFERENCE: A-70814/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/097, 100
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/953,351
PRIOR APPLICATION NUMBER: US 60/232,960
PRIOR APPLICATION NUMBER: US 60/232,960
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 461
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APPLICANT: Vega, Marioti
APPLICANT: Drittanti, Lila
APPLICANT: Flaux, Mariorie
TITLE OF INVENTION: MOTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES
FILE REPERENCE: 37851-912
CURRENT APPLICATION NUMBER: US/10/022,390
CURRENT FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72; DB 14; Length 461;
Pred. No. 0.0046;
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Pred. No. 0.0046;
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US-10-023-208-31

Sequence 31, Application US/10023208

Publication No. US20030124537A1

GENERAL INFORMATION:

APPLICANT: Li, Min

TITLE OF INVENTION: PROCARYOTIC LIBRARIES AND USES;

FILE REFERENCE: A-7017-41/RFT/RMS/RMK

FILE REFERENCE: A-7017-41/RFT/RMS/RMK

CURRENT APPLICATION NUMBER: US/10/023,208

CURRENT FILING DATE: 2001-12-17

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.1

LENGTH: 461

TYPEP: PRT
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PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 GSAVRVDQKCKGSVCIEPTP 251
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Best Local Similarity 70.0%;
Matches 14; Conservative 2
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US-10-023-208-31
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US-10-097-100-31
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US-10-080-376-31

US-10-080-376-31

Sequence 31, Application US/10080376

Publication No. US20020172968A1

GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE: A-70295-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US 09/792,630

PRIOR APPLICATION NUMBER: US 09/792,630

PRIOR PILING DATE: 2001-02-19

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.1

SEQ ID NO 31

LENGTH: 461
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Publication No. US20030049647A1
GENERAL INFORMATION:
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANT: DAHIYAT, BASSIL
APPLICANTON: UNGE OF NUCLEIC ACID LIBRARIES TO CREATE TOXICOLOGICAL
TITLE OF INVENTION: PROFILES
FILLE REFERENCE: XEN/001
CURRENT FILLING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/270,781
PRIOR PILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 0.0046;
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70.0%; Pred. No. v.v.
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                                                            232 GSAVRVDQKCKGSVCIEPTP 251
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                                1 GQAIRIDQKGKGSKQIEPTP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: goose parvovirus
US-10-080-376-31
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; ORGANISM: goose parvovirus
US-10-082-671-37
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Matches 14; Conserv
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US-10-082-671-37
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LENGTH: 461
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APPLICANT: Vega, Manuel
APPLICANT: Drittanti, Lila
TITLE OF INVENTION: HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS
FILE REPERENCE: 37851-911
CURRENT APPLICATION NUMBER: US/10/022,249
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR PILING DATE: 2001-08-27
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APPLICANT: Vega, Manuel
APPLICANT: Printanti, Lila
TITLE OF INVENTION: Marjorie
TITLE OF INVENTION: Marjorie
TITLE OF INVENTION: MUMBER: US/10/022,390
CURRENT APPLICATION NUMBER: US/10/022,390
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/315,382
PRIOR PILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 523
LENGTH: 621
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                                                                                                                         OTHER INFORMATION: Mutant rep protein: rep68 153 398 AGC GCG
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; OTHER INFORMATION: Mutant rep protein: rep78 153 398 AGC GCG
US-10-022-390-523
                                                                                                                                                                                      Score 72; DB 14; Length 536;
Pred. No. 0.0054;
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65.0%; Pred. No. o...
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 525 LENGTH: 536
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 525
LENGTH: 536
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 525, Application US/10022249
Publication No. US20030134351A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 523, Application US/10022390; Publication No. US20030129203A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                396 GSAVRVDQKCKSSAQIDPTP 415
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                                                                                  ORGANISM: Artificial Sequence
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ORGANISM: Artificial Seguence
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Best Local Similarity 65.0°
Matches 13; Conservative
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Matches 13; Conservative
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US-10-022-249-525
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US-10-022-390-523
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US-10-022-249-523

US-10-022-249-523

Sequence 523, Application US/10022249

Publication No. US20030134351A1

GENERAL INFORMATION:

APPLICANT: Vega, Manuel

APPLICANT: Dittant, Lila

TILE REFERENCE: 37851-91

CURRENT APPLICATION NUMBER: US/10/022,249

CURRENT FILING DATE: 2001-02-17

PRIOR APPLICATION NUMBER: 60/315,382

PRIOR PILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 735

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 523

LENGTH: 621
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Li, Min
APPLICANT:
Dahiyat, Bassil I.
TITLE OF INVENTION:
BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE:
A-70295/RFT/RMS/RMK
CURRENT APPLICATION NUMBER:
UNMBER OF SEQ ID NOS: 87
SOFTWARES: Patentin version 3.1
SEQ ID NO 29
LENGTH: 626
                                                       Gaps
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; OTHER INFORMATION: Mutant rep protein: rep78 153 398 AGC GCG
US-10-022-249-523
Score 72; DB 14; Length 621;
Pred. No. 0.0063;
3; Mismatches 4; Indels
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Job time: 34.75 secs
                                                                                                                                 396 GSAVRVDQKCKSSAQIDPTP 415
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                                                                                                     1 GOAIRIDOKGKGSKQIEPTP 20
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     Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative
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